

METHODS

5 This invention describes the production of genetically modified animals in which the genetic modifications are engineered in somatic cells cultured *in vitro* using the technique of gene targeting. Genetically modified cells are then used as nuclear donors to produce *inter alia*, live animals.

10 The methods described can also be used to validate loci in animal chromosomes which are suitable sites for transgene addition to cells. The method is particularly useful for cells that are required to have no unanticipated detrimental effect, such as cells destined for autologous transplantation.

15 The technique of nuclear transfer allows the production of offspring by the reconstruction of an early embryo. Genetic material from a donor cell or karyoplast is transferred to a suitable recipient cell from which the nuclear or genomic genetic material has been removed. In the first demonstrations of this technique, successful development was only obtained when the donor genetic material was taken from blastomeres from early embryos. Subsequently, development has been obtained using donor genetic material from differentiated cells maintained in culture and isolated from embryonic (Campbell *et al.*, Nature 380, 64-66, 1996), fetal and adult tissues (Wilmut *et al.*, Nature 385, 810-813, 1997); these reports form the basis of patent applications WO 97/07669 and WO 97/07668 which are incorporated into the present application in full, including all tables and diagrams.

25 Methods of nuclear transfer have also been described in published patent applications WO98/39416, WO98/30683, WO98/07841, WO97/37009, WO98/27214, WO99/01163 and WO99/01164.

30 Live offspring have been obtained in the mouse using quiescent cell populations derived directly *ex vivo* as nuclear donors (Wakayama *et al.*, Nature 394, 369-373

1998). The successful use of differentiated cells has also been demonstrated in sheep (Wilmot *et al.*, Nature 385, 810-813, 1997), cattle (Kato *et al.*, Science 282, 2095-2098, 1998; Wells, *et al.*, Theriogenology 1, 217, 1999; Zakhartchenko, *et al.*, Theriogenology 1, 218, 1999; Vignon, *et al.*, Theriogenology 1, 216, 1999) and mice (Wakayama *et al.*, Nature 394, 369-373).

In all the above cited references the nuclear donor and the recipient cell are taken from the same species. However, there has been success reported in achieving development from embryos reconstructed using nuclear donor and recipient cells from different species (Dominko, *et al.*, Theriogenology 49, 385, 1998; Mitalipova, *et al.*, Theriogenology 49, 389, 1998).

The use of nuclear transfer technology has many proven and potential benefits and uses in the production of mammalian embryos, fetuses and offspring. These include but are not limited to;

1. The ability to carry out genetic modification of cultured cells to be used as nuclear donors prior to embryo reconstruction.
2. The ability to carry out multiple genetic modifications in a single animal either by multiple genetic modifications of a cell population in culture or by sequential genetic modification, nuclear transfer and re-isolation of a cell population from the embryo, fetus or animal so produced.
3. The ability to increase the lifespan of cultured cell populations to be used for genetic modification by nuclear transfer and re-isolation of a cell population from the embryo, fetus or adult animal so produced.
4. The ability to produce multiple copies of an animal from a genetically modified, selected and cloned cell population.
5. The ability to produce multiple copies of any embryo, fetus or adult animal by nuclear transfer from cells taken directly *ex vivo*, or cell populations derived from any tissues taken from any of these stages with or without culture *in vitro*.

6. The ability to produce true clones (which share not only nuclear genetic identity, but also mitochondrial genetic identity) by utilising oocytes from the maternal line of the cell donor as cytoplasm recipients for embryo reconstruction.

5 7. The ability to store intact genomes for long periods (e.g. by freezing cell populations in liquid N₂) and to use these stored cells subsequently for the production of offspring by nuclear transfer.

8. The ability to dedifferentiate somatic nuclei and to produce undifferentiated cells that may be used to produce chimeric embryos, fetuses and adult animals by embryo aggregation, or injection. This can also be used to produce populations of embryonic stem, or embryonic germ cell populations.

9. The ability to dedifferentiate any somatic cell type by nuclear transfer and to isolate from the embryo so produced, embryonic stem cells, or any other desired specialised or unspecialised cell type e.g. neurones.

10 10. The possibility of achieving any of the objectives outlined in 1-9, by using nuclear donor and recipient cells from different species.

This process may be coupled with genetic manipulation techniques for the production of transgenic offspring (Schnieke *et al.*, Science 278, 2130-2133, 1997). The use of nuclear transfer coupled to genetic modification of cells in culture and their selection prior to animal production has a number of proven advantages, including;

1. Production of non-mosaic animals ensuring germ line transmission of the genetic modification/s (Schnieke *et al.*, *Supra*).

2. An increased efficiency in the production of such genetically modified animals (Schnieke *et al.*, *Supra*).

3. The production of multiple copies of the offspring thereby reducing the generation interval to produce flocks or herds of commercially important animals or increasing the numbers of animals for dissemination of genetic modification into the population as a whole (Cibelli, *et al.*, Nat. Biotechnol. 16, 642-6, 1998)

The existing and published nuclear transfer technology coupled to genetic modification of cells in culture provides animals containing single and multiple genetic modifications where the transgenes are incorporated at unselected locations within the host genome. However, the production of cultured cells which incorporate a desired genetic modification engineered at a precise and predetermined location in the host genome (gene targeting) has only been described previously in the art for the mouse using ES cells and the published methods do not involve nuclear transfer technology. No such equivalent methods exist for other mammals. Such modifications would have a number of advantages when applied to a variety of animal species including cattle, sheep, goats, horses, camels, rabbits and rodents. Such advantages include, but are not limited to:

1. The production of transgenic animals with superior transgene expression characteristics by placing the transgene at a predetermined site.
2. The removal, modification, inactivation or replacement of a chosen endogenous gene or genes and /or its control sequences.
3. If such modifications are found to have no unanticipated, detrimental effect on the resulting animal that could be ascribed to, for example, disruption of endogenous genes, activation of oncogenes, etc., this would constitute validation of the chosen locus as a preferred site for genetic modification, particularly if the site also conferred good expression of transgenes placed at the locus.

It is an objective of this patent specification to rectify this situation and describes for the first time, methods which can be utilised to produce such modified cells which can then optionally be used to make, *inter alia* whole animals by nuclear transfer. These methods (and others) can also be used to identify specific chromosomal loci as preferred targets for transgene addition as part of the process of *ex-vivo* gene therapy.

The present invention provides, according to a first aspect, a method of preparing a somatic cell for nuclear transfer, comprising modifying the genetic material of the

somatic cell by a genetic targeting event. Preferably the somatic cell is a primary somatic cell. The somatic cell is a vertebrate animal somatic cell. Preferably the cell is not an immortalised cell. Traditionally, cells can be defined as either "somatic", or "germ-line". Some cells, e.g. ES cells may not fall easily in either of these two traditional categories because they are derived from embryos before distinct somatic and germ lineages can be distinguished. Their functional equivalent, EG (Embryonic germ) cells are more easily defined as "germ-line" cells because they are derived from primordial germ cells. In the present text, the term "somatic" does not cover ES or EG cells.

The use of this method is not restricted to a particular donor cell type. Suitable cells include embryonic, fetal and adult somatic cells (of normal karyotype). In this text an "adult" cell or an "adult" animal is a cell or animal which is born. Thus an animal and its cells are deemed "adult" from birth. Such adult animals, in fact, cover animals from birth onwards, and thus include "babies" and "juveniles". The invention includes the use of undifferentiated e.g. somatic stem cells such as haemopoietic stem cells, at least partially differentiated and fully differentiated cells. Examples of partially differentiated cells include cells of embryonic lineage or precursor cells (e.g. neural precursor cells).

Suitable somatic cells according to the first aspect of the invention are preferably, but not necessarily, in culture. Suitable somatic cells include fibroblasts, epithelial cells, endothelial cells, neural cells, keratinocytes, hematopoietic cells, melanocytes, chondrocytes, lymphocytes (B and T), avian erythrocytes, macrophages, monocytes, mononuclear cells, cardiac muscle cells, other muscle cells, granulosa cells, cumulus cells and epidermal cells. The cells for the method of the first aspect of the invention may be obtained from a variety of different organs such as skin, mesenchyme, lung, pancreas, heart, intestine, stomach, bladder, major blood vessels kidney, urethra, reproductive organs etc. or a disaggregated preparation of a whole or part of a fetus or embryo.

Suitable cells may be obtained or derived from any animal, including birds such as domestic fowl, amphibian species and fish species. In practice however, it is mammalian animals that the greatest commercial advantage is envisaged. A preferred animal from which the somatic cell is obtained is an ungulate, selected from a bovid, ovid, cervid, suid, equid or camelid. In particular, the ungulate is a cow or bull, sheep, goat, bison, water buffalo or pig. Also contemplated by the present invention are somatic cells obtained or derived from a human, horse, camel, rodent (e.g. rat, mice) or a lagomorph (e.g. rabbit).

Suitable sources for recipient cells in the nuclear transfer process are not limiting. The recipient cell is preferably an oocyte, a fertilised zygote or a two cell embryo, all of which have been enucleated.

The genetic targeting event may be any which enables modification of the genetic material of the somatic cell at a predetermined site. Such a genetic targeting event includes inactivation, removal or modification of genetic material: upregulation of the function of genetic material; replacement of genetic material; and introduction of genetic material. The genetic material in particular comprises a gene or a part thereof or a region which influences the expression of a gene or genes. Accordingly, the genetic target events may include inactivation, removal or modification of a gene, upregulation of a gene, gene replacement or transgene replacement at a predetermined locus.

Preferably the genetic targeting event occurs by homologous recombination.

Preferably, the derivation of gene targeted cell clones occurs at high efficiency. According to this aspect of the invention, high efficiency is defined as a ratio of gene targeted:randomly transfected cell clones within the same selected cell population which is equal to or greater than 1:100.

The precise details of genetic targeting can be varied to improve the efficiency. In accordance with the variety of modifications, genetic targeting of a somatic cell suitable for nuclear transfer can be designed to maximise the frequency of homologous targeting. One factor which can be used to increase genetic targeting by homologous recombination is the effect of transcription on the target genetic material. Preferably, the genetic target is actively transcribed or is adjacent to a genetic locus which is actively transcribed. Such genetic targets or loci can be identified depending on the type of somatic cell used, and also possibly on the stage of such a cell. Such genes can be identified on the basis of the abundance of the corresponding mRNA molecules. Suitable genes would produce mRNAs which fall into the arbitrarily defined intermediate, or abundant class of mRNAs which are present at 300 or more copies of each molecule per cell (Alberts *et al.* 1994, Molecular Biology of the Cell, Garland Publishing, New York and London). An example of a suitable gene target in fibroblasts is any gene or locus encoding collagen, in particular the COLIA1 or the COLIA2 gene loci. However many suitable loci are present in a cell's genetic material.

According to this aspect of the invention, efficient means of transfection which maximises the number of cell clones derived which have undergone a gene targeting event may be used. For example, lipid mediated transfection reagents e.g. "LipofectaAMINE" (Gibco / Life Sciences) or "GenePorter" (Gene Therapy Systems) may be used.

Alternatively, or in addition, long regions of homology to the target locus may be included in the gene targeting vector. The total length of homology present in the targeting vector is preferably greater than 7kb.

Alternatively, or in addition, non-linear gene targeting vector DNA, *ie* DNA which has not been linearised by restriction enzyme cleavage, may be used. In this embodiment

of the invention, the DNA transfected is predominantly in a circular form, which may be substantially supercoiled or substantially relaxed.

5 The above features of the methods of transfection may be used alone or in combination with each other.

10 A particularly useful strategy to increase genetic targeting is the artificial induction of gene expression or induction of chromatin changes in a somatic cell type. Preferably the genetic targeting event is facilitated by an agent which inhibits histone deacetylation or by a factor which stimulates transcription at the target locus. The factor may be expressed in the host cell. This strategy is described in more detail in the remainder of this text.

15 In accordance with the genetic targeting of the present invention, it may be useful or necessary, at some point after the event and preferably before any nuclear transfer to remove portions of genetic material from the cell. Such material may be a selectable marker, or for example, an introduced genetic transcription activator. Such removal can be carried out by procedures described hereinafter , or by other procedures well known in the art.

20 The preparation of the somatic cell (by modification of the genetic material of the cell) may be a precursor step to nuclear transfer. The present invention provides, for the first time, a method by which a somatic cell can be genetically modified and which also supports successful nuclear transfer. Supporting successful nuclear transfer
25 requires that the reconstituted embryo proceeds to produce either a live born viable animal, or an embryo or fetus which can be used as a source of tissue, including EG cells and ES cells.

30 The method of nuclear transfer for the present invention is not limited. Any method of nuclear transfer may be used. The nuclear transfer may include genetic material from

one animal species or one animal type to a recipient cell of the same or different animal species or type.

5 A second aspect of the present invention provides a method of nuclear transfer, comprising a method of preparing a somatic cell for nuclear transfer (as set out in the first aspect of the invention) and a method comprising the transfer of the genetic material from the somatic cell to a recipient cell.

10 As described above, all and any method of nuclear transfer may be used according to the second aspect of the invention. The somatic cell may be as described above for the first aspect of the invention. The recipient cells may be any suitable recipient cell for any method of nuclear transfer, including an oocyte, a fertilised zygote or a two cell embryo which has been enucleated.

15 The transfer of the genetic material from a somatic cell to a recipient cell provides an animal embryo (the animal embryo comprises the single cell result of the nuclear transfer through to any and all multi-cell stage).

20 The method according to the second aspect of the invention may also comprise the production of cloned totipotent or pluripotent cells from an embryo or fetus derived by nuclear transfer. Methods for the derivation of totipotent or pluripotent cells, such as stem cells, from embryos (ES cells and ES-like cells) and from primordial germ cells of later stage embryos and fetuses (EG cells) have been described by many authors as cited later in this text. Pluripotent stem cells are particularly useful for the production
25 of differentiated cells and their precursors *in vitro* which may provide a source of cells for transplantation (preferably for humans).

Cells (including somatic cells) derived from embryos or fetuses (or adults) may also be used for further rounds of nuclear transfer. Rederivation of cells from an embryo or

fetus produced by nuclear transfer may facilitate multiple or sequential genetic manipulations which are otherwise not possible in the initial primary cells.

Alternatively, the method of obtaining an animal embryo according to the second aspect of the invention may further comprise causing an animal to develop to term from the embryo. In such a method, the animal embryo is preferably developed to term *in vivo*. If development up to blastocyst has taken place *in vitro*, then transfer into a surrogate animal takes place at this state. If blastocyst development has taken place *in vivo*, although in principal the blastocyst can be allowed to develop to term in the pre-blastocyst host, in practice the blastocyst will usually be moved from the temporary pre-blastocyst recipient and, after dissection from the protective medium, will be transferred to the permanent post blastocyst recipient. Development from the embryo to an adult goes through the stage of a fetus.

A third aspect of the invention provides a transgenic somatic cell, suitable for nuclear transfer, obtained by a method according to the first aspect of the invention.

A fourth aspect of the invention provides a transgenic embryo or fetus obtained by a method according to the second aspect of the invention.

A fifth aspect of the invention provides a method for preparing a transgenic animal comprising causing an animal to develop to term from an embryo or fetus according to the fourth aspect of the invention. Optionally, the transgenic animal of the fifth aspect may breed and such offspring (including embryos, fetuses and adults) are also encompassed by the present invention.

A sixth aspect of the invention provides a transgenic animal, or offspring thereof, according to the fifth aspect of the invention.

5 A seventh aspect of the invention provides a method for obtaining clonal pluripotent or totipotent cells (including a clonal pluripotent or totipotent cell population), the method comprising culturing a cell from a transgenic embryo or transgenic fetus, according to the fourth aspect of the invention, or from an adult developed from such an embryo or fetus.

An eighth aspect of the invention provides a clonal pluripotent or totipotent cell or cell population obtainable by a method according to the seventh aspect of the invention.

10 A ninth aspect of the invention provides a method for modifying the genetic material of a somatic cell while maintaining the totipotency of the cell, the method comprising a gene targeting event.

15 A tenth aspect of the invention relates to the use of artificial induction of gene expression or induction of chromatin changes prior to genetic targeting event. The genetic targeting event may be in any cell, including a somatic cell, a germ line cell, and ES cell and an EG cell. This aspect of the invention includes the artificial induction of gene expression or induction of chromatin changes in a cell, to either enable or increase the frequency of genetic targeting. The genetic targeting is
20 facilitated by the artificial induction of gene expression or by the induction of chromatin changes in a cell. Induction of chromatin changes may involve the use of agents which inhibit histone deacetylation (e.g. sodium butyrate or trichostatin A) to induce an open chromatin configuration and/or gene expression at the target locus before genetic targeting. The artificial induction of gene expression preferably
25 involves the use of an appropriate transcriptional activator. Such an activator may be a "factor" expressed in the host cell.

Details in respect of the artificial induction of gene expression or induction of chromatin changes to either enable or increase the frequency of gene targeting in a cell
30 are described later on in the present text. All details with respect to such genetic

targeting described in this text are included in this tenth aspect of the invention in as far as it relates not only to somatic cells, but also to germ line cells, to ES and to EG cells.

- 5 The tenth aspect of the invention includes the use of artificial induction of gene expression or induction of chromatin changes in any cell type in combination with nuclear transfer. Accordingly, the tenth aspect of the invention includes a method of preparing any cell type for nuclear transfer comprising the artificial induction of gene expression or induction of chromatin changes to facilitate a genetic targeting event.
- 10 Such a method may optionally also include transfer of genetic material from the cell into a suitable recipient cell (i.e. a nuclear transfer step). The method may be used to produce clonal totipotent or pluripotent cells and/or a transgenic embryo or animal. The totipotent or pluripotent cells may be obtained directly from cells after nuclear transfer or from the produced embryo or animal.
- 15 An eleventh aspect of the invention provides the use of an animal which has been obtained from a cell following a gene targeting event, to test for genetic changes due to the location of the gene targeting.
- 20 In accordance with this aspect of the invention, a selected cell (or population thereof) is (are) subjected to a gene targeting event. The gene targeting event may be as described according to the first aspect of the invention. The cell is then manipulated to provide an animal. The cell may be somatic or non-somatic. In the case of a somatic cell, the methodology used to regenerate an animal is preferably nuclear transfer and
- 25 the somatic cell is preferably a primary somatic cell. The cell may be a fibroblast. Details in respect of nuclear transfer are described above and references are given in the introductory portion of this text. Where the cell is other than a somatic cell (such as an ES or an EG cell) then the method of regenerating an animal may include nuclear transfer or other methods. Such other methods include blastocyst injection

and those described in Gene targeting: a practical approach. Ed Joyner, A.L. Oxford University Press, 1992 or in Stewart, Dev. Biol. 161, 626-628, 1994.

5 The phenotype of the animal reflects whether the desired effect of the gene targeting event has been achieved (for example, expression of the transgene) and also whether the gene targeting event has resulted in any detrimental effect which may be one or more genetic changes due to the location of the gene targeting. Such detrimental effects can include disruption of endogenous genes, activation of oncogenes, etc., and may manifest as physiological problems in the animal. The most serious detrimental effects include congenital disorders and an increase in the frequency of tumour formation. These effects can easily be identified by a consistent occurrence of the same problem in a set of clonally identical animals.

15 The animal produced (preferably a live born animal) is used to determine whether any detrimental effect has resulted from the genetic modification. The particulars of any one or more observed detrimental effect can be used to determine whether the loci identified is suitable for use in modifying cells. The determination of suitability will ultimately depend on the proposed use of cells which have been gene targeted at that locus. Where the locus is to be used to modify cells for human gene therapy, any detrimental effects must be minimal and not manifested in the cell type desired (e.g. for transplantation).

25 In accordance with the eleventh aspect of the invention, the use of an animal to test for genetic changes may be in relation to somatic and non-somatic cells. Non-somatic cells include ES and EG cells. Somatic cells include those described according to the first aspect of the invention. The cells may be from any animal, particularly a mammal. They may be derived directly or indirectly from an animal. Indirect derivation includes via stem cell differentiation or via therapeutic cloning. The cells for use with the eleventh aspect of the invention are not human. The cells are suitably derived from an animal which enables easy manipulation in genetic modification,

nuclear transfer and production to an animal. Since it is the animal produced which enables determination of a suitable locus, preferred animals may be those which are commonly handled for such procedures through nuclear transfer such as rodents (including mice), sheep and cattle.

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A twelfth aspect of the invention provides a method for validating a locus for targeting gene therapy comprising:

- obtaining cells of a chosen type;
- introducing a desired genetic change at a selected locus;
- growing a clonal population of the targeted cells; and
- demonstrating through the generation of an animal that the genetic change is acceptable.

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The cells may be as described for the eleventh aspect of the invention. The demonstration, preferably involves the production of a live born animal. As described above according to the eleventh aspect of the invention, the process of generating an animal may depend on the cells used for the genetic targeting. The process of producing an animal may include nuclear transfer or any other technique. For example, chimeric animals may be produced from ES or EG cells, in the first instance, followed by the production of a second generation animal, in which a parental genetic contribution from the original ES or EG cells is present in every cell.

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The determination of whether the genetic changes are acceptable will depend (as described for the eleventh aspect of the invention) on the intended use of any cells targeted at the locus. Preferably, the genetic changes cause no unexpected or undesired effects to the genome of the targeted cell. This is reflected in a healthy, live born animal.

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A thirteenth aspect of the invention provides for a validated locus, as identifiable according to the twelfth aspect of the invention. Such loci, once identified, can be used in any manner, including in the production of transgenic animals or in gene therapy as described herein.

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For all aspects of the invention, it is clear that more than one gene targeting event may take place. For example, in a single primary cell there may be a gene targeting event to remove or inactivate genetic material and a gene targeting event to introduce a transgene. More than two gene targeting events are also envisaged. The more than one gene targeting event may take place simultaneously, subsequently or sequentially in the same passage or a different passage. Alternatively a second or further gene targeting event may take place in a cell derived from an embryo, fetus or adult which was developed from an original somatic cell according to the present invention.

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The process of embryo reconstruction and production of viable offspring by nuclear transfer is a multistep procedure, each of these will now be described in detail. Also described are more details with respect to gene targeting according to the present invention. All details which follow apply to the invention herein described. In addition, the following terms are referred to in this text and their full expressions are set out here:

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ES cell - embryonic stem cell;

EG cell - embryonic germ cell;

MII - metaphase II;

PCR polymerase chain reaction;

HR - homologous recombination;

AAV - adeno associated virus;

DAF - decay accelerating factor;

MCP - membrane cofactor protein;

CD59 - membrane inhibitor of reactive lysis;
 HPRT - hypoxanthine phosphoribosyltransferase;
 gpt - xanthine guanine phosphoribosyltransferase;
 LIF - Leukaemia inhibitory factor;
 5 GFP - green fluorescent protein;
 IRES -internal ribosomal entry site
 AAT- alpha 1 antitrypsin
 BLG- beta lactoglobulin
 a1,3 GT- α 1,3-galactosyltransferase

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The Recipient Cell or Cytoplasm.

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Oocytes, fertilised zygotes and two cell embryos have been used as cytoplasm recipients for nuclear transfer. In general, oocytes arrested at metaphase of the second meiotic division (also termed unfertilised eggs, or MII oocytes) have become the cytoplasm of choice. At this point in oocyte development the genetic material is arranged upon the meiotic spindle and is easily removed using mechanical means. Several reports have demonstrated that during maturation i.e. between the germinal vesicle stage (prophase of the first meiotic division) and arrest at metaphase of the second meiotic division genomic DNA can be removed and the resulting cytoplasm used for nuclear transfer (Kato *et al.*, *Mol Reprod Dev* 36, 276-8, 1993). The use of fertilised zygotes as cytoplasm recipients has been reported in mouse (Kwon *et al.*, *Proc Natl Acad Sci U S A*, 93, 13010-3, 1996), cattle (Prather *et al.*, *J. Reprod Fertil Suppl* 41, 1990), and pigs (Prather *et al.*, *Biol. Reprod.* 41, 414-8, 1989). In cattle and pigs, development of embryos reconstructed using zygotes as cytoplasm recipients is low and on the whole restricted to the exchange of pronuclei suggesting that factors essential for successful development are removed with the pronuclei.

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Preparation of a Cytoplasm Recipient by Removal of the Genomic Genetic Material.

This process has in general been termed enucleation. In the majority of recipients
 utilised, the genomic DNA is not enclosed within a nuclear membrane at the time of
 removal. The removal of the genetic material according to the present invention and
 described by the term "enucleation" does not require that the genetic material is
 5 present in a nuclear membrane (it may or may not be, or may partially be).
 Enucleation may be achieved physically by actual removal of the nucleus, pronuclei or
 metaphase plate (depending on the recipient cell), or functionally, such as by the
 application of ultra-violet radiation or other enucleating influence. Removal of the
 genetic material is possible by physical and or chemical means. In the early reports of
 10 nuclear transfer, MII oocytes were simply cut in half on the basis that one half would
 contain the genetic material and the other would not. Modifications to this approach
 have been made in order to reduce the volume of cytoplasm, which was removed. This
 may be achieved by aspiration of a small amount of cytoplasm from directly beneath
 the 1st polar body using glass micropipettes or by using a knife to cut away that part of
 15 the oocyte beneath the polar body. To facilitate plasticity of the oocyte it may be pre-
 treated with cytochalasin B or other such agent that disrupts the cytoskeleton. In
 contrast to physical enucleation, chemical treatment has been demonstrated to cause
 complete removal of the genetic material in the mouse. Treatment of maturing oocytes
 with the topoisomerase inhibitor ectoposide results in the expulsion of all genomic
 20 material with the 1st polar body (Elsheikh *et al.*, Jpn J Vet Res 45, 217-20, 1998),
 however no development to term has been described using cytoplasm recipients
 produced by this method and there are no reports of this procedure in other species.
 Centrifugation of MII oocytes combined with Cytochalasin B treatment has been
 reported to cause enucleation in hamster and cattle oocytes (Tatham *et al.*, Hum
 25 Reprod 11, 1499-503, 1996). The development of embryos reconstructed from such
 cytoplasts has been reported in cattle however the frequency of development is low.

When using zygotes the genetic material may be removed by mechanical aspiration of
 both pronuclei. Dependent upon species, in order to facilitate visualisation of the
 30 pronuclei the zygotes may be centrifuged prior to enucleation.

Introduction of genetic material (embryo reconstruction).

Having prepared a suitable recipient cell or cytoplasm the donor genetic material must be introduced. Various techniques have been reported including;

- 5 1. Cell fusion induced by chemical, viral or electrical means.
2. Injection of an intact cell by any method
3. Injection of a lysed or damaged cell.
4. Injection of a nucleus.

Any of these methods may be used in any species or in a combination of species with some modifications of individual protocols.

Activation of the reconstructed embryo.

In addition to the transfer of donor genetic material from the karyoplast to the cytoplasm, the cytoplasm must be stimulated to initiate development. When using a fertilised zygote as a cytoplasm recipient, development has already been initiated by sperm entry at fertilisation. When using MII oocytes as cytoplasm recipients the oocyte must be activated by other stimuli. Various treatments have been reported to induce oocyte activation and promote early embryonic development including but not limited to; application of a DC electric stimulus, treatment with ethanol, ionomycin, inositol tris-phosphate (IP₃), calcium ionophore A23187, treatment with extracts of sperm or any other treatment which induces calcium entry into the oocyte or release of internal calcium stores and results in initiation of development. In addition any of these treatments in combination, their application at the same or different times or in combination with inhibitors of protein synthesis (i.e. cycloheximide or puromycin) or inhibitors of serine threonine protein kinases (i.e. 6-DMAP) may be applied.

Culture of reconstructed embryos.

Nuclear transfer reconstructed embryos may be cultured *in vitro* to a stage suitable for transfer to a final recipient using any suitable culture medium or culture process. The reconstituted embryos may otherwise be cultured *in vitro* until they are used in the

production of cloned totipotent or pluripotent cells, according to the second aspect of the invention. Alternatively, embryos may be cultured *in vivo* in the ligated oviduct of a suitable host animal (in general, sheep) until a stage suitable for transfer to a final surrogate recipient is reached in order for the animal to be grown to term. Embryos from cattle, sheep and other species may be cultured in a trans species recipient; for simplicity a sheep provides a suitable recipient for bovine, ovine and porcine species. It is usual to embed the embryos in a protective layer of agar or similar material to prevent mechanical damage to the reconstructed embryos or attack by macrophages whilst in the oviduct of the temporary recipient.

Gene targeting and embryonic stem cells

Gene targeting by homologous recombination between an exogenous DNA construct and cognate chromosomal sequences allows precise modifications to be made at predetermined sites in the genome. Gene targeting is well established in mouse embryonic stem (ES) cells, and has been used to effect modifications in a large number of murine genes (summarised by Brandon *et al.*, Curr. Biol. 5, 625-634, 758-765, 873-881, 1995). This has been facilitated by the ease with which genetic modifications engineered in ES cells *in vitro* can be transferred to whole mice and the consequences of gene targeting studied (reviewed by Papaioannou and Johnson, In: Gene targeting: a practical approach. Ed Joyner, A.L. Oxford University Press, 1992; and by Ramirez-Solis and Bradley Curr Opin. Biotech. 5, 528-533, 1994). Mouse ES cells are pluripotent cells derived from early embryos (Evans *et al.*, Nature 292, 154-156, 1981) which can be grown and manipulated *in vitro* then reintroduced into the preimplantation embryo where they can contribute to all cell types of a chimeric animal, including germ cells (Robertson, E.J., (Ed.) 1987. Teratocarcinomas and embryonic stem cells. A practical approach. IRL Press, Oxford.).

The potential benefits of engineering precise genetic modifications by gene targeting in species other than mice, e.g. livestock, have been described many times (e.g. Colman and Garner, Pharmaceutical Forum 5, 4-7, 1996). These include, but are not limited to, the production of human therapeutic proteins in the body fluids, disease

prevention, increasing required production traits, cell based therapies, cell based delivery systems for genetic therapy, tissue and organ transplantation.

5 Great efforts have therefore been made to derive ES lines from a wide variety of species. However, definitive ES cell lines i.e. capable of contributing to the germ line of a chimeric animal, have not been demonstrated from any mammalian species other than mouse. The status of human ES cells (Thomson *et al.*, Science 282, 1145-7, 1998), remains unknown in this respect because of ethical constraints. There are reports of ES or rather ES-like cell lines derived from hamster, mink, sheep 10 (Piedrahita *et al.*, Theriogenology 34, 879-901, 1990), cattle (Stice *et al.*, Biol. Reprod. 54, 100-110, 1996), pig (Gerfen *et al.*, Anim. Biotechnol. 6, 1-14, 1995) and rhesus monkey (Thomson *et al.*, Proc. Natl. Acad. Sci. USA 92, 7844-7848, 1995). In all of these cases, the more limited definition of "cells which under the appropriate *in vitro* conditions, can differentiate along at least three different lineages" has been used 15 to support claims that the cells derived represent ES cells. The production of pig (Wheeler, Reprod. Fertil. Dev. 6, 1-6, 1994) and rat chimeras have also been reported, although in neither case has ES contribution to the germ line been demonstrated.

Embryonic germ (EG) cells are undifferentiated cells functionally equivalent to ES 20 cells, that is they can be cultured and transfected *in vitro* then contribute to somatic and germ cell lineages of a chimera (Stewart, Dev. Biol. 161, 626-628, 1994). EG cells are derived by culture of primordial germ cells, the progenitors of the gametes, with a combination of growth factors: leukaemia inhibitory factor, steel factor and basic fibroblast growth factor (Matsui *et al.*, Cell 70, 841-847, 1992; Resnick *et al.*, Nature 25 359, 550-551, 1992).

Several attempts have been made to isolate EG lines from primordial germ cells in cattle (Cherny, *et al.*, Theriogenology 41, 175, 1994; Stokes, *et al.*, Theriogenology 41, 303, 1994), pig (Shim, *et al.*, Biol. Reprod. 57, 1089-1095, 1997; Piedrahita *et al.*, 30 Biol. Reprod. 58, 1321-1329, 1998) and rat (Mitani, *et al.*, Theriogenology 41, 258,

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1994). Blastocyst injection of cultured EG cells led to production of mid-gestation chimeric bovine embryos (Stokes, Theriogenology 41, 303, 1994). More recently chimeric male piglets have been produced from both genetically manipulated (Piedrahita, *et al.*, Biol. Reprod. 58, 1321-1329, 1998) and normal EG cells (Shim, *et al.*, Biol. Reprod. 57, 1089-1095, 1997). In both instances EG cell contribution to the testes was detected. Unfortunately the ability of this approach to achieve germline transmission could not be established, as one of the animals was stillborn and the other failed to thrive and was sacrificed.

10 The lack of fully functional large animal ES, or EG cells has however been circumvented by developments in nuclear transfer which allow genetic modifications to be made to somatic cells in culture and then those cells used as nuclear donors to produce a whole animal, as demonstrated by Schnieke *et al.* (*Supra*).

15 Gene targeting in somatic cells

There has been considerably less work on gene targeting in somatic cells.

The efficiency with which gene targeted clones can be derived is a function of the frequency of homologous recombination (HR) events and the frequency of random integration events. In all mammalian cell types, HR events are significantly less frequent than random events. Distinguishing HR events against a background of random integrants represents a major obstacle to the isolation of gene targeted clones. The results of published experiments indicates that gene targeting in somatic cells is infrequent, estimates of the ratio of HR to random events range from 1:50 or 1:230 in fibrosarcoma (Itzhaki *et al.*, Nat. Genet. 15, 258-265, 1997), 1:241 in myeloid leukemia cells (Zhen *et al.*, Proc. Natl. Acad. Sci. USA 90, 9832-9836, 1993), 1:1000 in bladder carcinoma (Smithies *et al.*, Nature 317, 230-234, 1985), to 1:9700 in erythroleukemia /lymphoblast fusion cells (Shesely *et al.*, Proc. Natl. Acad. Sci. USA 88, 4294-4298, 1991). However, these data were obtained from a range of

immortalised cell lines and describe the targeting of different gene loci with different gene targeting constructs.

In those few cases where the same construct has been used to target the same locus in both ES cells and somatic cells, the comparative data indicates that the ratio of HR to random integration events may be significantly lower in somatic cells (Arbones *et al.*, Nat. Genet. 6, 90-97, 1994). Recombinogenic cells of the immune system, such as B cells, represent a special exception (Buerstedde *et al.*, Cell 67, 179-188, 1991; Takata, M. *et al.*, EMBO J. 13, 1341-1349, 1994).

Comparison of the frequency of homologous recombination between immortalised and primary somatic cells indicates that homologous recombination is less frequent in primary cells than in immortalised cell lines (Finn *et al.*, Mol. Cell. Biol. 9, 4009-4017, 1989; Thyagarajan *et al.*, Nuc. Acids Res. 24, 4084-4091, 1996). This is important to the production of animals by nuclear transfer because normal, euploid, non-immortalised cells are preferred as nuclear donors because of the risk that immortalised cells may not support development or may lead to tumours in the resultant animal.

An undesirable consequence of a low frequency of homologous recombination is that it is necessary to transfect and screen large populations of the chosen cell type to ensure derivation of gene targeted cell clones. Although ES and EG cells can undergo extensive periods in culture and still be used to derive whole animals, primary cells have a limited lifespan in culture and their competence as nuclear donors may be reduced by genetic alterations which occur in vitro. This precludes the provision of large populations of primary cells by expansion in culture and extensive periods of culture to allow identification of gene targeted cell clones amongst a high background of random transfectants. Therefore there was an expectation that if gene targeting events did occur in primary cells the frequency of such events would be too rare to

allow the practical use of gene targeted cell clones to derive whole animals by nuclear transfer.

Factors affecting the frequency of gene targeting.

- 5 Numerous factors have been identified as affecting the frequency of gene targeting. As stated above, there are less data available regarding factors critical to targeting in somatic cells than ES cells.

- 10 The frequency of gene targeting in somatic cells has been shown to increase dramatically with the length of the region of homology in the targeting vector (Scheerer, *et al.*, Mol. Cell. Biol. 14, 6663-6673, 1994).

- 15 The use of DNA isogenic to the host cell has been demonstrated to improve the frequency of gene targeting in embryonic stem cells (Deng *et al.*, Mol Cell Biol. 12, 3365- 3371, 1992; te Riele *et al.*, Proc. Natl. Acad Sci. USA 89, 5128-5132, 1992). However this has not been investigated in somatic cells.

- 20 The effect of transcription of the target gene on the frequency of homologous recombination is the subject of some dispute. Some of the earliest reports of gene targeting demonstrated targeting modifications made to genes which are inactive in the cell type used (Smithies *et al.*, Nature, 317, 230-234, 1985; Johnson, *et al.*, Science 245, 1234- 1236, 1989). However, it has been proposed that homologous recombination at a gene locus is more frequent when that gene is actively transcribed than when it is inactive (Nickolof *et al.*, Mol. Cell. Biol. 10, 4837-4845, 1990; Thyagarajan *et al.*, Nucleic Acids Res. 23, 2784-2790, 1995). This proposal has been
- 25 disputed by Yanez and Porter, who report no correlation between gene targeting frequency and the transcriptional status of the interferon inducible 6-16 gene in human HT1080 cells (Gene Therapy, 5, 149-159, 1998).

The presence of double strand breaks at the target locus has been shown to stimulate gene targeting in CHO cells (Liang *et al.*, Proc. Natl. Acad Sci. USA 93, 8929-8933, 1996) but not mouse Ltk⁻ cells (Lukacsovich *et al.*, Nuc. Acids Res. 22, 5649-5657, 1994). However double strand breaks have also been shown to stimulate the level of illegitimate recombination in CHO cells (Sargent *et al.*, Mol Cell Biol. 17, 267-277, 1997). The consequent risk of introducing genetic aberrations reduces the usefulness of this approach for cells destined for nuclear transfer. This also applies to other methods of stimulating homologous recombination by induction of DNA damage, e.g. chemical carcinogens, UV radiation, gamma radiation and photoreactive molecules (reviewed by Yanez and Porter, Gene Therapy, 5, 149-159, 1998).

There is a widespread perception by researchers in the field that to achieve gene targeting, vector DNA should be introduced into the host cell by either electroporation, or more rarely by microinjection. A survey of the extensive literature describing gene targeting (summarised by Brandon *et al.*, supra) indicates that electroporation is by far the method preferred in the art.

The art also teaches that linearising the gene targeting vector before it is introduced into the host cell dramatically increases the frequency of gene targeting (reviewed by Yanez and Porter, supra). Again a survey of the literature describing gene targeting indicates that gene targeting vectors are used in linear form. Therefore the expectation was that use of linear DNA would be required for gene targeting in somatic cells for all target loci in somatic cells.

Yanez and Porter (supra) also review other factors which affect the rate of homologous recombination. These include the growth conditions of the host cell culture, the stage of the cell cycle of the host cell, modification of the ends of linearised transfected DNA, the inactivation of the MSH2 gene and the inhibition of poly ADP ribose polymerase enzyme activity.

Methods of enriching or identifying gene targeting events

There are several methods whereby cells carrying possibly rare targeting events can be enriched, or identified from a transfected population.

5 Transfectants can be divided into pools and the presence of targeted clones within each pool screened, typically by the polymerase chain reaction. Positive pools are then progressively subdivided and rescreened until a single clone has been isolated (Shesely, *et al.*, Proc. Natl. Acad. Sci. USA 88, 4294-4298, 1991). However, as
10 mentioned previously, such schemes are unsuited to primary cells destined for nuclear transfer, because repeated rounds of purification extend the time in culture. Extended culture is undesirable because primary cells may become senescent or acquire genetic aberrations.

The use of gene targeting vectors which maximise the target frequency and allow
15 selection of targeted clones without increasing the time spent in culture is more appropriate for cells destined for nuclear transfer. Gene targeting strategies such as the enhancer trap, promoter trap and polyadenylation trap are described in detail by Hasty and Bradley (In: Gene targeting: a practical approach. Ed Joyner, A.L. Oxford University Press, 1992) and are discussed later in this text.

20

Other gene targeting methods

Very high rates of homologous recombination have been reported using chimeric RNA/DNA oligonucleotides for targeting the β -globin gene in lymphoblastoid cells (Cole-Strauss, Science 273, 1386-1389, 1996) and the Factor IX gene both *in vitro* and
25 *in vivo* (Kren, *et al.*, Nature Med. 4, 285-290, 1998). Unfortunately the technology does not seem to transfer easily and other researchers have failed to apply it to their gene of choice (Strauss, Nature Medicine 4, 274-275, 1998).

High targeting frequencies have also been observed with gene targeting vectors based on the adeno-associated virus (AAV). Russell *et al.* (Nature Genetics 18, 325-330, 1998) report 11 out of 13 transfected primary human fibroblasts had a correctly targeted hypoxanthine phosphoribosyltransferase gene.

5

Both of these methods are limited in the type of modification that can be engineered, because only a few nucleotide changes can be made at the target locus. While this allows gene inactivation e.g. by the insertion of stop codons, or subtle modification by the substitution of individual amino acids, these methods do not allow the insertion or replacement of larger regions which are necessary for gene replacement or transgene placement.

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In this text, there is described the generation, identification and isolation of somatic cells carrying predetermined genetic modifications at a defined locus, "gene targeting" while maintaining the ability of those cells to support production of, following nuclear transfer, either i) a fetus or ii) a viable animal or iii) pluripotent cell populations.

15

While the method is applicable to all mammalian species, the preferred species are sheep, cattle (cow and bull), goat, pig, horse, camel, rabbit, rodent and human. This invention does not relate to human reproductive cloning. It does cover human tissue cells and, where applicable, human embryos, in particular, embryos under 14 days old.

20

Preferably, gene targeting is carried out at, or adjacent to, a gene locus which is actively transcribed, or otherwise capable of supporting gene targeting at high frequency. Also preferred is the use of an efficient lipid mediated transfection system e.g. "GenePorter" (Gene Therapy Systems). The use of a gene targeting vector DNA in supercoiled or circular form is also preferred. Long regions of homology to the target locus may be included in the vector. Combinations of these preferred methods of gene targeting are within the scope of the invention. For example, in a particularly preferred embodiment, the use of a lipid mediated transfection system in combination

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with a gene targeting vector in circular form (relaxed and/or supercoiled) can achieve efficient gene targeting at gene loci which are poorly transcribed or inactive in the host cell.

5 Many somatic cell types are capable of supporting nuclear transfer and are thus suitable according to the present invention (e.g. mammary epithelial cells, muscle cells, fetal fibroblasts, adult fibroblasts, oviduct epithelial cells, granulosa cells and cumulus cells). Many other cell types will also support nuclear transfer, including embryonic stem cells and their differentiated derivatives, endothelial cells and sub-
10 endothelial cells. Gene targeting of somatic cells in combination with nuclear transfer allows more flexibility than gene targeting using ES cells alone. ES cells are a single cell type which display a single pattern of gene expression. The wide choice of somatic cells available for nuclear transfer allows a cell type to be chosen for gene targeting in which the gene locus of interest is preferably transcriptionally active, or
15 capable of supporting gene targeting at high frequency. Thus, the frequency of homologous recombination can be maximised.

This strategy can be extended to include the artificial induction of gene expression or induction of chromatin changes in a somatic cell type to either enable or increase the
20 frequency of gene targeting. Induction of chromatin changes may involve the use of agents which inhibit histone deacetylation (e.g. sodium butyrate or trichostatin A) to induce an open chromatin configuration and/or gene expression at the target locus before gene targeting.

25 Gene expression and histone acetylation

There is strong evidence that gene activity is correlated with the acetylation of core histones (reviewed by Jeppeson, Bioessays, 19, 67-74, 1997; Pazin and Kadonaga, Cell 89, 325-328, 1997) and that histone deacetylation regulates gene transcriptional activity (Wolffe, Science 272, 371-372, 1996). Detailed mechanisms of repression
30 involving proteins with histone deacetylase activity have been elucidated for several

genes (e.g. Brehm *et al.*, Nature 391, 597-601, 1998; Magnagi-Jaulin *et al.*, Nature 391, 601-604, 1998; Iavarone *et al.*, Mol Cell Biol 19, 916-922, 1999). The inhibition of histone deacetylase activity by chemical reagents such as sodium butyrate, or trichostatin A has been shown to reactivate silent genes (Chen *et al.*, Proc. Natl. Acad. Sci. USA 94, 5798-5803, 1997) and inhibit transcriptional repression (Brehm *et al.*, Nature 391, 597-601, 1998; Magnagi-Jaulin *et al.*, Nature 391, 601-604, 1998). The effect of inhibitors of histone deacetylase on the frequency of gene targeting has not been described in the art.

Alternatively, particular genes or classes of genes can be activated using particular transcriptional activators. Such transcriptional activators may be termed "factors". For example, Weintraub *et al.* (Proc. Nat. Acad. Sci. USA, 86, 5434-5438, 1989) show that primary human and rat fibroblasts, when transfected with the transcriptional activator, MyoD, turn on a variety of muscle genes, and in the case of the rat cells, can form myotubes. Likewise, Tontonoz *et al.* (Cell, 79, 1147-1156, 1994) have shown that the regulators PPAR γ and C/EBP α synergise to powerfully promote adipogenesis in fibroblasts. In the context of the protocols described in this text, targeting to genes which are normally active in muscle or fat cells can be effected by the introduction of the type of factors described above. However, it is important that the method used to introduce a transcription factor does not compromise the ability of the cells to support nuclear transfer.

Expression of transcription factors can be achieved by transient transfection of an expression construct prior to gene targeting. Because only a small proportion of cells transiently transfected actually integrate the exogenous DNA into their genome, a transcription activator designed to effect activation of a gene at the target locus can be expressed prior to gene targeting and will in the majority of cells leave no integrated DNA. The presence or absence of integrated transcription activator construct DNA can be determined in individual clones and those which lack integrated copies used for nuclear transfer. Where necessary, integrated copies of transcription activator

expression constructs can be removed if they are flanked by recognition sites for site specific recombinase enzymes e.g. the *loxP* sites for Cre or the FRT sites for FLP recombinase (Kilby *et al.*, Trends in Genetics, 9, 413-421, 1993).

- 5 The choice of target locus may be made on the basis of the ability of that locus to support gene targeting at high frequency, or on the basis of the function of the gene. Gene targeting at the target locus may be carried out so that the expression of the target gene is reduced or ablated, increased, or left unaffected. Gene targeting does not necessarily have to affect the function of the target gene, indeed in some
- 10 circumstances it may be preferable that expression and function of the target locus is left unaffected.

- Gene targeting of primary somatic cells is carried out to achieve gene inactivation, gene upregulation, gene modification, gene replacement, or transgene placement at the
- 15 target locus. Examples of preferred target loci and modifications include, but are not limited to:

1. inactivation, removal or modification
 - of genes responsible for the presence of antigens which are xenoreactive to humans
 - 20 (e.g. α -1,3 galactosyltransferase),
 - of the PrP locus responsible for the production of the prion protein and its normal counterpart in non human animals,
 - of genes which in humans are responsible for genetic disease and which in modified, inactivated or deleted form could provide a model of that disease in animals, e.g. the
 - 25 cystic fibrosis transmembrane conductance regulator gene.
 - of regulatory regions or genes to alter the expression of one or more genes, e.g. RFX transactivator genes which are responsible for regulation of major histocompatibility class II molecules
 - of endogenous viral sequences

- of genes responsible for substances which provoke food intolerance or allergy.
- of genes responsible for the presence of particular carbohydrate residues on glycoproteins, e.g. the cytidine monophospho-N- acetyl neuraminic acid hydroxylase gene in non-human animals
- 5 - of genes responsible for the somatic rearrangement of immunoglobulin genes, e.g. RAG1, RAG2

2. upregulation

- of genes responsible for suppression of complement mediated lysis (e.g. porcine CD59, DAF, MCP)
- 10 - of gene expression by the introduction of a response element to allow experimental modulation of gene expression

3. gene replacement

- 15 - replacement of genes responsible for production of blood constituents (e.g. serum albumin) with their human counterpart.
- replacement of genes responsible for substances which provoke food intolerance or allergy with a more benign (e.g. human) counterpart
- replacement of immunoglobulin genes with their human counterpart.
- 20 - replacement of genes responsible for surface antigens with their human counterpart.

4. transgene placement at a predetermined locus:

- placement of a transgene at a gene locus which may offer advantageous transgene expression
- 25 - placement of a transgene at a site which places it under the control of an endogenous regulatory region.

The gene targeting vector and the experimental procedure is designed so that the time taken to identify, isolate, analyse and expand primary cell clones carrying targeted events is minimised. This is an important aspect of the invention because reduction of

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the time in culture increases the likelihood that cells used as nuclear donors are viable, normal and euploid. Recognised risks associated with *in vitro* culture of primary cells which are detrimental to the outcome of nuclear transfer include: senescence due to limited lifespan, acquisition of genetic damage, loss of a normal complement of chromosomes and rapid erosion of chromosomal telomeres.

Precautions which can optionally be taken to minimise the time in culture are:

1. Cryopreservation of cell samples destined for use as nuclear donors at the earliest possible stage.
2. The use of a gene targeting vector which allows direct selection or identification of homologous recombinants relative to random integrants.
3. The use of culture conditions designed to reduce the metabolic insults suffered by the primary cells. For example, by the use of a reduced oxygen atmosphere, or the inclusion of antioxidants to minimise the extent of oxidative damage. However, the invention is not limited to the use of such conditions.

The use of promoter trap, or polyadenylation trap strategies (reviewed by Hasty and Bradley In: Gene targeting: a practical approach. Ed Joyner, A.L. IRL press Oxford, 1992) are preferred embodiments of the invention. In each case, the gene targeting vector is designed such that homologous recombination between the gene targeting vector and the target locus renders a marker gene active, while in the majority of random integrants it is inactive. Marker genes may include genes which confer resistance to drugs (e.g. neomycin, G418, hygromycin, zeocin, blasticidin, histidinol) or other selectable markers (e.g. HPRT, gpt), visible markers (e.g. GFP) or other selection systems (e.g. single chain antibody /hapten systems; Griffiths *et al.*, Nature 312, 271-275, 1984). Conversely, strategies may be designed such that homologous recombination results in removal of a negatively selectable marker gene. For example a vector could be designed such that in correctly targeted cells a site specific recombinase gene e.g. the Cre or FLP recombinase (Kilby *et al.*, Trends in Genetics, 9, 413-421, 1993) is activated e.g. by a promoter or polyadenylation trap, and the

recombinase results in the deletion of a toxin gene flanked by appropriate recognition sites (e.g. *loxP* or FRT sites)

5 The gene targeting vector is designed to maximise the frequency of homologous targeting relative to random integration events. This is achieved by incorporating large regions of DNA homologous to the target locus into the gene targeting vector. While it is desirable to maximise the size of these homologous regions, in practice these are limited by the constraints of construct production and the requirement for a reliable, simple genetic screen (e.g. by PCR amplification) to identify targeted events.

10 Homologous DNA in the gene targeting vector may, or may not be isogenic to the host cell, in that it may or may not be derived from the host cell, or from other cells of the same individual.

15 Gene targeting can be carried out such that a transgene is cointegrated with a selectable marker gene at the target locus. This could be used to provide a suitable site for achieving high expression of the transgene. A preferred embodiment of the invention is the placement of a transgene designed to express a foreign protein in the milk of a transgenic animal at a locus known, or predicted to support abundant expression in the mammary gland. This can be achieved by, for example, placing a

20 structural gene adjacent to the endogenous promoter of a milk protein gene. Another example is the placement of a gene adjacent to the endogenous promoter of a collagen gene. Where the presence of the marker gene is undesirable in the final animal, it may be removed by the action of specific recombination systems e.g. the Cre/*loxP* system or the FLP/FRT system (Kilby *et al.*, *Supra*) if it is flanked by recombination

25 recognition sites. Removal of the marker gene may either be achieved in the cells before nuclear transfer, or in cells derived from animals (including fetuses) produced by nuclear transfer, or in oocytes, zygotes, or embryos which carry the genetic modification and are from a lineage which started with an animal made by nuclear transfer or during subsequent mating of animals derived by nuclear transfer. A

30 method whereby Cre recombinase can be specifically activated and used to effect

recombination during the production of male gametes has been described by O'Gorman *et al.*, (Proc. Natl. Acad. Sci. USA. 94, 14602-14607, 1997).

5 Multiple rounds of gene targeting may be carried out, either in cells before nuclear transfer or in cells derived from an animal produced by nuclear transfer. Retargeting of a locus may be facilitated by the inclusion of a marker gene in the first round of targeting such that its loss on subsequent targeting allows ready identification or selection of clones carrying subsequent targeted events.

10 As stated earlier, one part of the present invention provides for the generation of animals which contain targeted modifications to their genomes. Not all regions of the genome are suitable sites for modification because of their proximity to gene silencing elements such as those seen in heterochromatin and because modification to certain sites can have disruptive effects on endogenous gene expression. These potential
15 undesirable consequences can be examined in any animals resulting from the nuclear transfer process, particularly those homozygous at the targeted locus (loci). This can be achieved by backcrossing or by using nuclear donors where the same targeting event has been achieved at both alleles. It has been claimed that a significant proportion of a preferred embodiment of the invention is the validation of target loci as
20 preferred sites for genetic modification because of the absence of collateral genetic damage and their ability to confer good levels of transgene expression as assessed in nuclear transfer animals. Such a validation would be extremely valuable for those contemplating *ex-vivo* gene therapy.

25 *Ex-vivo* gene therapy.

Ex vivo gene therapy is a means of delivering therapeutic gene products to a patient in which cells derived by biopsy, are manipulated *in vitro* and then returned to the same patient. Gene therapy by transplantation of *ex vivo* genetically engineered cells has been used for both local and systemic delivery of proteins to experimental animals.
30 For example, Hortelano *et al.*, (Human Gene Therapy 10, 1281-8, 1999) and Regulier

et al., (Gene Therapy 5, 1014-1022, 1998) describe the transplantation into mice of myoblasts expressing human clotting Factor IX and erythropoietin respectively. Cao et al (J. Mol Med 76, 782-789, 1998) and Muller-Ladner et al. (Arthritis. Rheum. 42, 490-497, 1999) describe the transplantation into mice of fibroblasts expressing cytokines and cytokine inhibitors respectively.

To date, the choice of cell used for ex-vivo gene therapy is dictated by its availability from the patient, the ease with which genetic manipulation can be carried out, etc. If adult stem cells were available more readily, these would provide suitable targets for gene manipulation, either because of their abilities to form a self sustaining population or because they can be induced to differentiate in vitro into cell type difficult to access from the patient e.g. neurons (see Smith, Current Biology R802-804, 1998). More recently, there have been proposals that a similar objective could be obtained using therapeutic cloning (Trounson and Pera Reprod Fertil Dev 10 121-125 1998). Therapeutic cloning is an as yet untried application of nuclear transfer which promises to provide cells, tissues, and organs for a human patient requiring replacement or supplementation of diseased or damaged tissue. In outline, somatic cells are obtained by biopsy, their nuclei transferred into an oocyte, human blastocysts derived and used to produce embryonic stem (ES) cells, or other pluripotent cells, which are then induced to differentiate into the cell type required for transplantation. If nuclear donor cells are obtained from the patient requiring the transplant this would provide an autologous graft. Preferably, gene targeting would be performed on the somatic donor population prior to therapeutic cloning since all cells from the disaggregated embryo would have the desired alteration thereby minimising time needed in culture to expand cell populations prior to transplantation.

Genetic modification of cells destined for human transplantation. Although, in some instances, healthy, unmanipulated cells would suffice, the function and efficacy of tissue produced by either therapeutic cloning, or ex vivo gene therapy would require, or be enhanced by genetic modification. Genetic modification could be

used to effect changes to endogenous genes in situ e.g., to repair or remove a genetic defect, or to add a transgene. Transgenes may be added to achieve a variety of therapeutic goals, the precise nature of which would depend on the condition to be treated and the cells to be transplanted. For example, a transgene could be designed to:

- 5 - aid the longevity of the transplanted cells
- aid the interaction of the transplanted cells with the host tissue
- aid terminal differentiation of transplanted precursor cells
- induce regeneration of host tissue, e.g. by expression of a growth factor
- express a factor which is deficient, absent or sub-functional in the patient
- 10 - facilitate controlled ablation of transplanted cells if required
- to act as a source of agent toxic to cells close to the site of transplantation, e.g.
 for cancer treatment.

While effecting changes in endogenous genes can only be achieved by gene targeting,
15 transgene addition can be achieved by either random integration, or gene targeting. However, gene targeting offers several important advantages over random integration as a means of adding a transgene to cells destined for human transplantation.

Transgenes integrated at random in a host genome are subject to the well documented
20 “position effect”. This can lead to suboptimal transgene expression and may subject the transgene to influences capable of disturbing the tissue or temporal pattern of gene expression and which are necessarily unpredictable. In contrast, gene targeting allows the precise placement of a transgene at a predetermined locus which can be chosen to provide desirable expression characteristics.

25 Integration of a transgene into some sites in the host genome may physically disrupt structural gene sequences, or lead to aberrant up or down-regulation of endogenous gene expression. Random integration therefore carries a risk of causing a deleterious phenotype in the host cell, including tumorigenesis. Gene targeting, however, allows

the placement of a transgene at a predetermined site which can be chosen on the basis of its safety in this respect.

5 Although the frequency of gene targeting in somatic cells is generally regarded as very low compared to the frequency of random integration, we demonstrate in this patent specification that an appropriate combination of target locus, host cell type and targeting vector can lead to a very high frequency of targeting.

10 Desirable criteria for a target locus for transgene placement can therefore be summarised as below:

1. The locus should support transgene expression at abundant levels should it be required.
2. The locus should not unduly influence the tissue specific regulation of the transgene.
- 15 3. Transgene integration at the target locus should have minimal or no effect on cell phenotype.
4. The target locus should support gene targeting at high frequency, preferably in cells which are readily obtained by biopsy and which can be cultured, transfected and drug selected. A high frequency of gene targeting is desirable as it simplifies the
20 experimental procedures and would minimise the amount of tissue required from the patient by biopsy and would minimise the time needed for in vitro culture.

Our findings, as fully described in the examples, indicates that the COLIA1 locus represents an example of a good target locus in these respects.

25 A major application of *ex vivo* gene therapy is the use of genetically modified transplanted cells as a means of providing a protein lacking in the patient, for example blood clotting factors for haemophiliac patients. A primary objective of genetic manipulation of such cells is to achieve a suitable level of expression of the
30 therapeutic product in the transplanted cells. This can be accomplished by the

placement of a transgene as a discrete transcription unit at a target locus under the control of a promoter optimally active in the cell type in which transgene expression is desired. However, an alternative approach is to place the transgene under the control of an endogenous gene promoter, a promoter which directs abundant expression in the cell type transplanted would be particularly suitable for expression of a protein required in large amounts or where the number of cells transplanted into the patient is restricted. For example, the endogenous promoter may direct expression in fibroblast cells or in endothelial cells. The transgene can be placed under the control of the endogenous promoter without disturbing the expression of the endogenous gene by inserting the transgene sequence within the 3' untranslated region of the mRNA such that it forms part of a bicistronic message. Translation of the transgene coding region can be achieved by insertion of an internal ribosomal entry site. The successful placement of a marker transgene as part of the COLIA1 mRNA is described in the examples.

Nuclear transfer as a test of a cells normality after gene targeting

An important aspect of this invention is the demonstration that normal viable animals can be derived by nuclear transfer from cell clones which have undergone transgene placement by gene targeting at the COLIA1 locus.

Production of an animal by nuclear transfer provides a very stringent test of the normality of the donor cell. Thus, nuclear transfer in animals such as sheep provides a rigorous means of testing gene targeting procedures before they are carried out in human cells destined for transplantation therapy. We have identified that gene targeting and nuclear transfer in animals such as sheep offers a means of identifying target loci suitable for human gene targeting. The value of nuclear transfer in a particular animal species as a test of the safety of an equivalent human locus would be greatest in regions where a high degree of synteny exists between the human and animal genome.

Means of identifying human target loci suitable for transgene placement and those target loci are encompassed within the scope of this invention. Because the same loci could be used to place different transgenes in a range of therapeutic applications, a set of candidate target loci identified by animal nuclear transfer animal can be characterised further, for example in human cell culture before they are used for human therapy.

This information can be applied to the choice of targeting site for gene therapy. Whatever the choice of cell type used, it will be imperative that the population used all have the same, pre-selected modification. This will involve cell cloning from correctly modified primary differentiated or stem cell types. Where therapeutic cloning is used all the cells will by origin, have the same genotype.

All preferred features of each aspect of the invention apply to all other aspects *mutatis mutandis*.

The following drawings are referred to in the present text:

Figure Legends

Figure 1

Structure of the COLT-1 gene targeting vector and the targeted ovine COLIA1 locus

The upper portion shows a diagram of the COLT-1 vector with the 5' and 3' regions homologous to the ovine COLIA1 locus, the IRES neo region and the bacterial plasmid indicated.

A double crossover event at the ovine COLIA1 locus (middle) results in the structure of the targeted locus as indicated in the lower portion of the figure. Although it is not possible to determine the precise sites where recombination between the COLT-1

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vector and the target locus recombination occur, regions at the target locus homologous to the COLT-1 vector are shown in darker shading.

Figure 2

- 5 PCR screening strategy used to identify gene targeting events at the ovine COLIA1 locus.

10 The upper portion shows the approximate position of the two primers used to amplify a 3.4 fragment from a region unique to the COLT-1 vector to a region unique to the COLIA1 locus.

Sequence A shows a portion of DNA sequence spanning the junction between the region unique to the COLIA1 locus and the 5' region of shared homology with the COLT-1 vector. The position and orientation of the COLTPCR4 primer is shown.

15 Sequence B shows a portion of DNA sequence spanning the junction between the IRES neo gene and the 5' region of shared homology. The position and orientation of the COLTPCR8 primer is shown.

20 Figure 3

Agarose gel electrophoresis of PCR fragments amplified from COLT-1 transfected G418 resistant PDFF-2 cell clones. Lanes containing samples from cell clones 1, 2, 6, 12, 13, 14, and 26 are indicated. The position of the diagnostic 3.4kb amplified fragment is indicated by the arrow.

25

Figure 4

Sequence analysis of the 5' junction of the targeted ovine COLIA1 locus in three independently derived targeted cell clones.

The upper portion shows the sequence of the 5' end of the linearised COLT-1 gene targeting vector. Terminal sequence derived from a cloning vector is indicated

5 The middle portion shows a portion of the sequence of the diagnostic 3.4 kb fragment amplified from each of the targeted cell clones 6, 13 and 14 spanning the junction between the region unique to the COLIA1 locus and the 5' region of shared homology with the COLT-1 vector.

10 The lower portion shows the sequence of the PDFF2 COLIA1 locus over the same region.

Figure 5.

Construction of COLT-2 transgene placement vector

15 The upper portion of the diagram shows the structure of the BLG driven AAT transgene inserted into the COLT-1 vector. The middle shows the COLT-1 vector and the point at which the AATC2 transgene was inserted. The lower portion of the diagram shows the structure of the COLT-2 vector. Functional regions of each construct are distinguished by patterns and shading and are as indicated.

20

Figure 6

Southern analysis of COLIA1 gene targeted lambs.

25 Lanes indicated in the key contain genomic DNA from lambs derived by transfer of nuclei from cell clones targeted by COLT-1 (PDCOL6) and COLT-2 (PDCAAT90), control DNA samples from a normal lamb, cell clone PDCAAT90 and non transfected PDFF2 cells. The positions of the 7kb fragment derived from the non-targeted COLIA1 locus and the 4.73 kb fragment derived from the targeted COLIA1 locus are indicated by arrows.

30

Figure 7

The structure of the ovine COLIA1 locus and the COLT-1 and 2 targeting vectors and COLT-1 and 2 targeted loci are shown.

5 The diagram of the COLIA1 locus shows the position of the translational stop and polyadenylation sites and the direction of COLIA1 transcription as an arrow. The asterisk shows the position of the SspI restriction site where the targeted gene insertions were made. The position of the COLIA1 probe used for Southern analysis in Figures 6 and 8 is shown.

10

The IRES neo cassette is indicated by a shaded box, the bacterial vector pSL1180 is indicated by an open box and the BLG driven AAT transgene by a striped box. The diagrams of the targeted loci show the direction and predicted extent of the COLIAI / IRES neo bicistronic message and also the AAT message as arrows.

15

The scale of the diagram is indicated by the 2kb scale bar. Restriction enzyme sites shown are: K, KpnI; A, AspI; Sc, SacII; S, Sall; B, BamHI.

Figure 8

20 Southern analysis of COLT-2 transfected (PDCAAT) cell clones.

The identity of each cell clone is shown above each lane. Those which provided a positive signal by PCR are indicated. Also included are non transfected PDFF-2 cells. The positions of the 7kb fragment derived from the non targeted COLIA1 locus and
25 the 4.73 kb fragment derived from the targeted COLIA1 locus are indicated by arrows.

Figure 9

Northern analysis of total RNA derived from PDCAAT cell clones 81 and 90 and non transfected PDFF-2 cells.

30

The source of each RNA sample is indicated over each lane. The left upper autoradiograph shows hybridisation to a neomycin phosphotransferase (neo) probe, the right upper autoradiograph shows hybridisation to a human COLIA1 probe. The lower two panels show hybridisation to a mouse α -actin probe. The position of the 28S and 18S ribosomal RNA bands are indicated.

Figure 10

Northern analysis of primary ovine mammary epithelial (POME) cells in culture.

POME cells were grown for a total of 4 and 9 days in culture on either fibronectin (FN) or type I collagen coated dishes. Cells were either grown continuously in Proliferation Medium (uninduced) or grown for the final three days before harvest in Induction Medium (induced). Total RNA was extracted and subjected to Northern analysis using standard procedures. The autoradiograph shows the result of hybridisation with an ovine beta lactoglobulin (BLG) probe. The source of each RNA is indicated above each lane. Total RNA prepared from the mammary gland from which the cells were derived is also included. The size and position of the ovine BLG mRNA is indicated by the arrow.

Figure 11

The structure of the ovine beta lactoglobulin (BLG) locus and the BLAT-3 targeting vector are shown.

The diagram of the BLG locus shows the position of the BLG translational start (ATG), stop and polyadenylation sites and the direction of transcription from the BLG promoter. Exons are indicated by black boxes. Exon 3 at which the targeted insertion is designed to take place is marked. The position of the primers used to PCR amplify a fragment from the targeted locus is indicated. The 5' and 3' regions of the BLAT-3 vector homologous to the ovine BLG locus are marked. The IRES neo cassette is

indicated by a shaded box and the bacterial vector pBS (Bluescript) indicated by an open box. The scale of the diagram is indicated by the 2kb scale bar.

Figure 12

5 Agarose gel electrophoresis of PCR fragments amplified from BLAT-3 transfected G418 resistant POME cell clones. Lanes containing samples from BLAT-3 transfected POME cell clones 1-16 are indicated. Also included is a fragment amplified from a plasmid constructed to mimic the 5' structure of the BLAT-3 targeted BLG locus, marked as "positive control". Non transfected POME cells are also indicated. The
10 position of the 2.375kb diagnostic fragment is shown by the arrow.

Figure 13

Schematic map of the porcine α 1,3 GT promoter-trap knockout vector pPL501 and 502. Porcine α 1,3 GT genomic structure was based on the report by Katayama et al
15 (Katayama, A et al, Glycoconjugate J , 15, 583-589, 1998). The gene is 24 kb in size, and contains 6 exons and 5 introns; The start codon is located in exon 4.

Figure 14

Outline of the PCR screening strategy for the detection of homologous recombination events at the porcine α 1,3 GT locus. Small arrows indicate the positions of the two
20 PCR primers. The subcloned 2.4 kb PCR fragment was sequenced from both ends.

Figure 15

Sequence analysis over the 3' junction region of the PCR fragment amplified from
25 porcine α 1,3 GT targeted cell clones.

The upper portion shows the sequence of the portion of the circular gene targeting vectors pPL501 and 502 at the 3' end of the 3' homologous arm or each. The junction

between the 3' region of homology to the porcine α 1,3GT gene and bacterial plasmid sequence is indicated.

5 The lower portion shows the sequence of the diagnostic 2.65 kb fragment amplified from four of the targeted cell clones spanning the junction between the region unique to the 1,3-GT locus and the 3' region of shared homology with the α 1,3-GT gene targeting vector. The sequence derived from each clone was identical.

Figure 16

10 Schematic map of bovine BLG poly A-trap knockout vector. 5' homologous recombination arm is a 10kb fragment of BLG promoter. 3' homologous recombination arm is a 1.9kb fragment containing BLG exon 2 to intron 3.

Figure 17

15 PCR screening and DNA sequencing of BLG knockout clones. The 5' primer, Neo442s, is located at 3' end of neo gene. The 3' primer, BLG3'1, is approximately 260bp 3' of the 3' end of the 3' homologous arm. The PCR product from the targeted locus is .

20 Figure 18

Sequence analysis over the 3' junction region of the PCR fragment amplified from three bovine BLG targeted cell clones.

25 The upper portion shows the sequence of the portion of the circular gene targeting vector pPL522 at the 3' end of the 3' homologous arm of each. The junction between the 3' region of homology to the bovine BLG gene and bacterial plasmid sequence is indicated

The lower portion shows the sequence of the diagnostic 2.3kb fragment amplified from three of the targeted cell clones spanning the junction between the region unique to the BLG locus and the 3' region of shared homology with the BLG gene targeting vector. The sequence derived from each clone was identical.

5

We have demonstrated gene targeting at three gene loci in three species. In each case the frequency of gene targeting achieved was significantly in excess of the rate that could be expected in primary cells based on published data.

- 10 The sheep COLIA1 locus has been targeted by placement of a selectable marker gene alone and in combination with a transgene. The COLIA1 gene expresses the alpha-1(I) procollagen gene at high level in the fibroblast cells used for targeting. The frequency of gene targeting obtained with the marker gene was slightly greater than 1 targeted event per 10 drug resistant cell clones. This is significantly in excess of the rate of
- 15 gene targeting that could be expected in primary cells based on published data. Furthermore, the cells carrying the targeted modification retained their ability to support nuclear transfer and the production of viable lambs has been demonstrated. This therefore facilitates the practical use of somatic cells coupled with nuclear transfer as a means of transferring precise predetermined genetic modifications
- 20 wrought *in vitro* to whole animals.

The sheep beta lactoglobulin gene has been targeted at high efficiency in primary cells chosen because they provided abundant expression at the target locus.

- 25 The pig alpha 1,3-galactosyltransferase gene has been targeted in primary fibroblasts which were estimated to express at the target locus at low level. Targeting was achieved using a novel method of transfection suited to gene targeting at gene loci which are transcribed at low level, or are inactive in the host cell type.

The bovine beta lactoglobulin gene has been targeted at high efficiency in primary fibroblasts which do not detectably transcribe the target locus, using the same novel method of transfection.

5 The present invention is exemplified by the following, non-limiting examples.

Example 1

Placement of a neo marker gene at the COLIA1 locus in primary ovine fetal fibroblast cells by gene targeting

10

The Poll Dorset primary fetal fibroblast primary culture PDFF2 has been described previously (Schnieke *et al.*, *Supra*). PDFF2 genomic DNA was used to generate a library of cloned DNA fragments from which a molecular clone corresponding to a portion of the ovine COLIA1 gene from exon 44 to approximately 14 kb 3' of the translational stop site was isolated. The ovine COLIA1 molecular clone was used as a

15

COLT-1 is designed to place the neo selectable marker gene downstream of the COLIA1 gene without disrupting the expression of the COLIA1 gene.

20

Gene targeting with the COLT-1 vector was designed to maximise the frequency of homologous recombination in PDFF2 fetal fibroblasts:

a. The choice of target locus, COLIA1 gene locus is highly expressed in fibroblasts.

b. The COLT-1 construct was designed as a promoter trap such that the construct alone does not confer G418 resistance. Homologous recombination at the COLIA1 locus introduces a neo gene lacking a promoter but which has at the 5' end an internal ribosomal entry site (IRES) to facilitate translation. Homologous recombination results in insertion of the IRES neo gene into the COLIA1 transcribed region downstream of the COLIA1 translational stop site. Transcription of the targeted COLIA1 locus

25

produces a bicistronic message with translation of the neo coding region occurring by initiation at the internal ribosomal entry site.

c. The length of the regions within COLT-1 homologous to the COLIA1 gene was maximised.

5

COLT-1 consists of:

A 3 kb region of the 3' end of the ovine COLIA1 gene, from a position approximately 2.9kb 5' of the translational stop site to an SspI site 131 bases 3' of the stop site.

10 A 0.6 kb internal ribosomal entry site (IRES) region corresponding to bases 1247 to 1856 of the IRES hygro vector (Clontech, Genbank accession number: U89672)

A 1.7 kbp region containing the bacterial neo gene and a portion of the 3' end of the human growth hormone gene containing the polyadenylation site essentially the same as that described by McWhir *et al.*, (Nature Genetics 14, 223-226, 1996)

15 A 8.3 kb region of the 3' end and flanking region of ovine COLIA1 gene, from a SspI site 131 bases 3' of the translational stop site to a XhoI site approximately 8.4kb 3' of the stop site.

The bacterial cloning vector pSL1180 (Pharmacia)

20 The structure of the COLT-1 Vector and the targeted COLIA 1 locus are shown in Figure 1.

COLT-1 DNA linearised with the restriction enzyme SalI was transfected into early passage PDFF2 cells and G418 resistant cell clones were isolated as summarised below:

25

Day 0: 5×10^5 cells PDFF2 cells at passage 3 were transfected with 6µg linearised COLT-1 DNA using lipofectAMINE following the procedure recommended by the manufacturers (Gibco, BRL Life Technologies).

Day 2: Transfected cells were split into two sets of eight (10cm) dishes and G418 added to the medium at either 0.8 mg/ml, or 3.0 mg/ml.

5 Day 11-18: Colonies were isolated and replated into 6 well dishes. Samples were taken for PCR analysis.

Day 15- 19 Colonies were expanded into 25cm² flasks. Further samples were taken for PCR analysis

10 Day 20-25 Expanded clones were cryopreserved.

Throughout, PDFF-2 cells were grown in BHK 21 (Glasgow MEM) medium supplemented with L-glutamine (2mM), sodium pyruvate (1mM) and 10% fetal calf serum in standard tissue culture flasks and dishes in a humidified tissue culture incubator using an atmosphere composed of 2% O₂, 5% CO₂, 93% N₂. Cells were
15 passaged by standard trypsinisation.

PCR analysis was used to distinguish between random integrated copies of COLT-1 and homologous recombinants at the COLIA1 locus. The PCR scheme used is shown
20 in Figure 2. The upper part of Figure 2 shows the predicted structure of the targeted locus and the positions of the two primers used to amplify a fragment of 3.4kb if the IRES neo cassette is inserted at the correct position in the COLIA1 gene. The DNA sequences A and B, in the lower part of the figure, show the precise positions of each primer relative to the structure of the targeted locus.

25 Samples of cells to be screened were lysed in PCR lysis buffer (50mM KCl, 1.5 mM MgCl₂, 10mM Tris pH8.5, 0.5% NP40, 0.5% Tween) plus proteinase K, and incubated at 65°C for 30min. Proteinase K was inactivated at 95°C for 10 min and polymerase chain reaction carried out using the "Expand long template PCR system" (Boehringer)

following the manufacturers recommended conditions. Thermal cycling conditions were as below:

5	10 cycles of	94°C	2 min
		94°C	10 sec
		55°C	30 sec
		68°C	2 min
		20 cycles of	
10		94°C	10 sec
		60°C	30 sec
		68°C	2 min + 20 sec/cycle
		68°C	7 min

Figure 3 shows a representative agarose gel electropherogram of PCR products amplified from seven G418 resistant cell clones. Four of these (clones 6, 13, 14, 26) show the presence of the diagnostic 3.4 kb fragment indicative of integration of the IRES neo gene into the COLIA1 locus by homologous recombination.

In total 63 clones were analysed by PCR, 7 of which (11%) were positive.

The nucleotide sequence of fragments amplified from three clones (6, 13, 14) was determined and compared with the sequence of the ovine COLIA1 gene. Portions of the sequence of the fragment amplified from each clone is shown in Figure 4. It can be seen that in each case the sequence of the fragment amplified from each clone is identical over the 5' junction of the targeted locus and is consistent with a homologous recombination event occurring between the COLT-1 plasmid and the endogenous COLIA1 gene. That is, the PCR fragment contains sequence from the COLIA1 gene 5' of that present within the COLT-1 construct and does not contain the sequence known to be present at the extreme 5' end of the linearised COLT-1 construct.

Example 2. Generation of COLT-1 gene targeted sheep

Targeted clones 6 and 13 were selected for nuclear transfer primarily because they grew most readily in culture. The chromosome number of these clones was determined as a basic requirement for competence as nuclear donors. In each case the gross chromosome number indicated that each clone was euploid.

Table 2 shows the chromosome number of clones 6 and 13

Clone	number spreads counted	number spreads 53/54 ¹
6	28	17
13	42	28

¹ Number of spreads with a chromosome count of either 53 or 54.

It was calculated that the total period of culture these cells had undergone since disaggregation of the original fetus up to the point of preparing multiple cryopreserved stocks ready for rounds of nuclear transfer was 30 days. This period was made up of four stages: 2 days and 3 days for the initial establishment of the PDFF-2 working stock of primary cells, 20 days during which time gene targeting was carried out, and 5 days for the expansion of the clones and provision of multiple stocks for nuclear transfer. Between these stages cells were stored by cryopreservation.

Cryopreserved stocks of each cell clone were thawed, grown for 1-2 days then prepared for nuclear transfer as below.

Preparation of cells to act as nuclear donors.

Donor cells were plated at 2×10^4 cells per well of a 6 well tissue culture dish and cultured for 16-24 hours in BHK 21 (Glasgow MEM) medium supplemented with L-glutamine (2mM), sodium pyruvate (1mM) containing 10% fetal calf serum. At 24

hours the medium was aspirated and the cell monolayer was washed three times in medium containing 0.5% fetal calf serum. Cultures were then incubated at 37°C in low serum medium (0.5%) for 2-5 days until they had exited the cell cycle as determined by staining for proliferating cell nuclear antigen (PCNA) in control cultures.

Cells were harvested by trypsinisation and stored in suspension in medium containing 10% fetal calf serum for 2-3 hours prior to use as nuclear donors.

10 Superstimulation of donor ewes and recovery of oocytes

Ewes to act as oocyte donors were synchronised with progestagen sponges for 14 days (Veramix, Upjohn, UK) and induced to superovulate with single injections of 3.0 mg/day (total 6.0 mg) ovine follicle-stimulating hormone (FSH) (Ovagen, Immunochemical Products Ltd. New Zealand) on two successive days. Ovulation was induced with an 8 mg single dose of a gonadotropin-releasing hormone analogue (GnRH Receptal, Hoechst. UK.) 24 hours after the second injection of FSH.

Unfertilised metaphase II oocytes were recovered by flushing from the oviduct at 24-29 hours after GnRH injection using Dulbecco's phosphate buffered saline containing 1.0% fetal calf serum (FCS) maintained at 37°C until use.

Oocyte manipulation.

Recovered oocytes were maintained at 37°C, washed in phosphate buffered saline (PBS) 1.0% FCS and transferred to calcium free M2 medium containing 10% Foetal Calf Serum (FCS), at 37°C. To remove the chromosomes (enucleation) oocytes were placed in calcium free M2 containing 10% FCS, 7.5 µg/ml Cytochalasin B (Sigma) (Cytochalasin B is optional) and 5.0 µg/ml Hoechst 33342 (Sigma) at 37°C for 20 minutes. A small amount of cytoplasm from directly beneath the 1st polar body was then aspirated using a 20 µM glass pipette. Enucleation was confirmed by exposing

the aspirated portion of cytoplasm to UV light and checking for the presence of a metaphase plate.

Embryo reconstruction.

5 Groups of 10-20 oocytes were enucleated and placed into 20 μ l drops of calcium free M2 medium at 37 $^{\circ}$ C, 5% CO $_2$ under mineral oil (SIGMA). At 32-34 hours post hCG injection, a single cell was placed into contact with the enucleated oocyte. The couplet was transferred to the fusion chamber (see below) in 200 μ l of 0.3 M mannitol, 0.1mM MgSO $_4$, 0.001mM CaCl $_2$ in distilled water. Fusion and activation were induced by
10 application of an AC pulse of 3V for 5 seconds followed by 3 DC pulses of 1.25kV/Cm for 80 μ sec. Couplets were then washed in TC199 10% FCS (the addition of 7.5 μ g/ml Cytochalasin B to this medium is optional) and incubated in this medium for 1 hour at 37 $^{\circ}$ C, 5% CO $_2$. Couplets were then washed in TC199 10% FCS and cultured in TC199 10% FCS at 37 $^{\circ}$ C, 5% CO $_2$ overnight. Alternatively, the donor
15 nucleus may be transferred by either manual or piezo-electric aided injection or by any other chemical or physical means of producing cell fusion.

Embryo culture and assessment.

After the overnight culture period fused couplets were double embedded in 1% and
20 1.2% agar (DIFCO) (or any other suitable protective covering material) in PBS and transferred to the ligated oviduct of synchronised ewes. After 6 days recipient ewes were sacrificed and the embryos retrieved by flushing from the oviduct using PBS, 10% FCS. Embryos were dissected from the agar chips using 2 needles and development assessed by microscopy. All embryos which had developed to the
25 morula/blastocyst stage were transferred as soon as possible to the uterine horn of synchronised final recipient ewes.

Nuclear Transfer: births from COLT-1 targeted sheep.

Results of nuclear transfer using two COLT-1 targeted clones, termed PDCOL6, and
30 13 are summarised in Table 3.

Table 3. Nuclear transfer using COLT-1 targeted cell clones

	PDCOL 6	PDCOL 13
No. reconstructed embryos	109	154
No. embryos recovered from temp. recipient	104	149
No. embryos developed to morula or blastocyst	14	43
No. embryos transferred to final recipients	14	43
No. recipients	8	22
No. fetuses detected at day 60 by ultrasound scan	5*	10*
No. liveborn lambs	4	8
No. lambs surviving more than 1 month	2	2

* one twin pregnancy

5

Southern analysis of one still born and one live lamb derived from cell clone PDCOL6 are shown in Figure 6. The hybridisation probe used was a 3kb COLIA1 fragment which constitutes the 5' region of homology present in vectors COLT-1 and 2 which reveals a 4.73 kb band diagnostic of the targeted allele and a 7kb band from the non-targeted allele. The upper part of Figure 7 shows the structure of the COLT-1 targeted

10

locus showing the position of the hybridisation probe used for Southern analysis and the origin of the fragments seen in Figure 6.

These data indicate that each lamb analysed showed the presence of both wild type and targeted alleles.

Example 3. Placement of a transgene at the COLIA1 locus in primary ovine fetal fibroblast cells by gene targeting.

The construct COLT-2 is shown in Figure 5. COLT-2 was generated by insertion of a MluI fragment containing the AATC2 transgene expression cassette into a unique EcoRV site situated at the 3' end of the IRES neo segment of COLT-1.

AATC2 consists of the 5' portion of the vector pACTMAD6 (described in patent application WO 99/ 03981), comprising the ovine β -lactoglobulin promoter and mouse cardiac actin 1st intron, linked to human α -1 antitrypsin cDNA and the 3' portion of the pMAD vector (described in patent application WO 99/ 03981), comprising the ovine β -lactoglobulin exon 7, polyadenylation site and 3 flanking region.

COLT-2 DNA linearised with the restriction enzyme SacII was transfected into early passage PDFF2 cells and G418 resistant cell clones were isolated in the manner described for COLT-1 transfection in Example 1.

The time course of the experiment is shown below:

Day 0: 30 μ g COLT-2 DNA transfected into PDFF2 cells at
passage 2 in 5 X 25cm² flasks

- Day 2: transfected cells plated onto 80 X 10cm diameter petri dishes and 0.8 mg/ml G418 selection applied
- Day 11-12: 384 vigorous G418 resistant colonies picked to individual wells of 6-well dishes.
- 5 Day 15: 104 clones sampled for PCR analysis
- Day 15: 15 vigorous PCR +ve clones passed to 25cm² flasks
- Day 18: 15 clones cryopreserved

10 Seventy of the 104 cell samples were screened by PCR using the same method as COLT-1. This yielded 46 positive signals, indicating a targeting efficiency of 66%. Cell clones derived from COLT-2 targeting were termed PDCAAT.

15 Southern analysis of a group of PCR positive PDCAAT cell clones and one PCR negative clone is shown in Figure 8. The autoradiograph shows the results of hybridisation with a 3kb COLIA1 fragment which constitutes the 5' region of homology present in vectors COLT-1 and 2. A diagram of the structure of the COLT-2 targeted locus showing the position of the hybridisation probe and the origin of the fragments is shown in Figure 7.

20 The COLIA1 probe hybridised to a 4.73 band diagnostic of the targeted allele and a 7kb band from the non-targeted COLIA1 allele. It can be seen that PDCAAT cell clones 22, 71, 73, 81, 84, 89, 90, 92 and 95 show the presence of both fragments in equimolar ratio, consistent with the targeting of one COLIA1 allele. Clone 86 shows only the non-targeted allele consistent with the negative PCR result. Clones 87 and 99

25 show the presence of the targeted and non-targeted alleles and additional bands which could represent either rearrangements at the target locus, or random integration events. It is not known whether these indicate the presence of both random and targeted events within the same cell clone, or that these cultures are oligoclonal. Clone 78 shows the presence of the targeted fragment at a lower intensity than the non-targeted fragment

again perhaps indicating that this is not a pure clone. DNA from clones 59 and 125 was uncut.

Northern analysis of COLT-2 targeted cell clones

5 Cell clones PDCAAT 81 and PDCAAT 90 were grown to confluence in 75cm² flasks, total RNA extracted and Northern analysis carried out by standard procedures. Duplicate samples of 10 µg of each RNA were subjected to gel electrophoresis using a formaldehyde agarose gel and MOPS running buffer. After transfer, the membrane was cut in half to provide two filters for Northern analysis. One half was hybridised
10 with a 4.1 kb human COLIA1 cDNA followed by hybridisation with mouse β-actin cDNA. The other half filter was hybridised with a neomycin phosphotransferase probe and then with mouse β-actin cDNA. Results are shown in Figure 9.

Transcription of the COLT-2 COLIA1 targeted locus was predicted to produce a
15 bicistronic message, with the IRES-neo portion fused to the COLIA1 transcript after the stop codon. The results shown in Figure 9 are consistent with this. The right upper autoradiograph (hybridisation to collagen cDNA) shows a single mRNA species of approximately 4.8 kb, as estimated by the position of the 28s rRNA, corresponding to the endogenous COLIA1 mRNA. Interestingly, although both mice and human show
20 two endogenous COLIA1 mRNA species from different poly A sites, sheep show a single species. A larger species is present in the PDCAAT clones 81 and 90, consistent with the size (~6.8 kb) predicted for the COLIA1 IRES-neo fusion mRNA. The left upper autoradiograph shows hybridisation to the neo probe. The single mRNA species detected in PDCAAT 81 and 90 is the size predicted for the bicistronic message. No
25 mRNA species were detected with the neo probe in non-targeted PDFF-2 cells. Hybridisation with mouse β-actin cDNA was used as an indication of the amount of RNA loaded in both filters and is shown in the lower two panels.

Northern analysis was also carried out to investigate whether insertion of the AATC2 transgene at the COLIA1 locus led to expression of BLG directed AAT expression in fibroblasts. Hybridisation with an human α 1-antitrypsin probe was used to detect expression of the transgene. No AAT mRNA was detectable in PDFF-2, PDCAAT81 or PDCAAT90 cells. It can therefore be concluded that insertion of the transgene at the COLIA1 locus does not induce significant leaky expression of BLG-driven AAT in fibroblasts.

Example 4. Generation of a sheep carrying a transgene placed at the COLIA1 locus.

Karyotype analysis of three PDCAAT cell clones derived in Example 3 was carried out as a basic requirement for competence as nuclear donors. In each case the gross chromosome number indicated that each clone was euploid. Table 4 shows the chromosome number of cell clones PDCAAT81, 90 and 95.

Table 4. Chromosome numbers in PDCAAT cell clones

Clone	number spreads counted	number spreads 53/54 ¹
81	31	26
90	35	34
95	24	18

¹ Number of spreads with a chromosome count of either 53 or 54.

PDCAAT cell clones 81 and 90 were used for nuclear transfer using the method described in Example 2. Results of nuclear transfer are summarised in Table 5.

Table 5. Nuclear transfer using COLT-2 targeted cell clones

	PDCAAT 81	PDCAAT 90
No. reconstructed embryos	71	83

No. embryos recovered from temp. recipient	62	78
No. embryos developed to morula or blastocyst	4	19
No. embryos transferred to final recipients	4	19
No. recipients	2	10
No. fetuses detected at day 60 by ultrasound scan	2	3*
No. liveborn lambs	0	2
No. lambs surviving more than 1 month	0	1

* one twin pregnancy

Genomic DNA was prepared from tissue biopsies from lambs obtained by nuclear transfer. Southern analysis of one still born and one live lamb derived from cell clone PDCAAT90 are shown in Figure 6. The diagnostic fragments observed (see Figure 7) confirm the presence of the wild type and targeted allele in each case.

Example 5. Targeting of a gene locus in cells chosen to provide abundant expression at the target locus.

The ovine beta lactoglobulin (BLG) gene is specifically expressed in the ovine mammary gland in late pregnancy and during lactation. Gene targeting at this locus was achieved by choosing an appropriate host cell type. These were primary mammary epithelial cells which express BLG at high level in culture.

Preparation of primary ovine mammary epithelial (POME) cells

All procedures were carried out under sterile conditions

- 5 1. Mammary tissue was excised from a 115 day pregnant ewe and cut into 5cm pieces removing fat and major blood vessels.
2. The pieces of mammary tissue were washed 3 times with fresh Dissection Medium in a laminar flow cabinet hood and cut into 1cm pieces.
- 10 3. The tissue pieces were injected with Dissociation Medium until the tissue became distended.
- 15 4. Tissue was minced into a paste and transferred to a conical flask and 4ml Dissociation Medium were added per g of tissue.
5. Tissue was incubated in a rotary shaker (~200 rpm) at 37 deg. C for 1-5hr until the tissue passed easily through a wide bore Pasteur pipette.
- 20 6. A series of differential centrifugation steps were used to enrich the epithelial component of the mammary tissue.
 - a. Cell suspension centrifuged at 100 rpm, 30 sec
 - b. Floating fat aspirated and discarded
 - 25 c. Pellet redigested for a further 30-60 min and step a repeated.
 - d. Supernatant centrifuged at 800 rpm, 3 min
 - e. Floating fat aspirated and discarded
 - f. Pellet resuspended in Proliferation Medium
 - g. Supernatant centrifuged at 1500 rpm, 10 min
 - 30 h. Supernatant discarded

i. Pellet resuspended in Proliferation Medium

7. Pellets from steps 6f and i were combined and cells were seeded at 2.5×10^5 cells/cm² onto either collagen (Sigma C8919) or fibronectin (Sigma 4759) coated tissue culture flasks in Proliferation Medium containing 50µg/ml gentamycin (Sigma G1397).

8. Induction of milk gene expression in POME cells was carried out by growth of confluent monolayers for 3 days in Induction Medium

10

Media used in POME cell preparation and culture

Dissection Medium

M199 (Gibco/BRL 22340-020)	500ml
100x antibiotic/antimycotic (Gibco/BRL 15240-039)	10ml
50mg/ml gentamycin (Sigma G1397)	0.5ml

15

Dissociation Medium

M199 (Gibco/BRL 22340-020)	500ml
NaHCO ₃ (Sigma S5761)	0.6g
Trypsin (Gibco/BRL170702-018)	0.75g
Collagenase A (Boehringer 1088-793)	1.5g
Fetal calf serum	25ml

20

Proliferation Medium

(1:1) DMEM/F12 (Gibco/BRL 4196-039, 21765-029)	500ml
Fetal calf serum	50ml
5mg/ml bovine insulin (Gibco/BRL 13007-018)	0.5ml
10 g/ml epidermal growth factor (Sigma E4127)	0.5ml
5mg/ml linoleic acid (Sigma L8384)	0.5ml

30

Induction Medium

	(1:1) DMEM/F12 (Gibco/BRL 4196-039, 21765-029)	500ml
	Fetal calf serum	50ml
	5mg/ml bovine insulin (Gibco/BRL 13007-018)	0.5ml
5	5mg/ml linoleic acid (Sigma L8384)	0.5ml
	5mg/ml ovine prolactin (Sigma L6520)	0.5ml
	1mM dexamethasone (Sigma D4902)	0.5ml

BLG expression and induction in cultured POME cells

- 10 Expression of BLG was analysed in POME cells grown for a total of 4 and 9 days in culture. Cultures of POME cells were grown on either fibronectin (FN) or type I collagen coated dishes. Cells were either grown continuously in Proliferation Medium or subjected to induction of milk gene expression by growth for three days in Induction Medium. Total RNA was extracted and subjected to Northern analysis using
- 15 standard procedures.

Figure 10 shows Northern analysis of POME cell cultures. The filter shown was hybridised with an ovine BLG probe. It can be seen that all cultures express abundant quantities of BLG mRNA at day 4 with a slight reduction after 9 days in culture.

- 20 Analysis of POME cells at later stages showed further reductions in BLG expression. This highlighted the need to carry out gene targeting in POME cells within a short period after derivation. POME cells which had been cryopreserved directly after derivation behaved in a similar manner and could be used conveniently.

- 25 The mRNA detected in this Northern analysis represents transcriptional activity of the BLG gene in culture and not mRNA residual from the mammary gland because induction significantly increased the amount of BLG message present in each case.

Generation of a BLG promoter trap vector BLAT-3

BLAT-3 is a promoter trap gene targeting vector designed to disrupt expression of the ovine BLG gene by insertion of an IRES neo cassette into exon 3.

BLAT3 consists of:

5 A 1.84kb region of the 5' end of the ovine BLG gene from a SacI site 25 bases 5' of the translational start to a ClaI site within exon 3.

A 0.6 kb internal ribosomal entry site (IRES) region corresponding to bases 1247 to 1856 of the IRES hygro vector (Clontech, Genbank accession number: U89672)

10 A 1.7 bp region containing the neo gene (encoding neomycin phosphotransferase) and a portion of the 3' end of the human growth hormone gene containing the polyadenylation site, essentially the same as that described by McWhir *et al.*, (Nature Genetics 14, 223-226, 1996)

15 An approximately 12 kb region of the ovine beta-lactoglobulin gene from a ClaI site within exon 3 to a point approximately 9kb 3' of the polyadenylation site corresponding to the end of a genomic clone in phage lambda.

The structure of the BLAT-3 vector and the position of PCR primers used to detect targeting events are shown in Figure 11.

20 Targeting of BLG in POME cells using vector BLAT-3

BLAT-3 DNA linearised with SalI was transfected into early passage POME cells and G418 resistant clones derived as described below:

25	Day 0	6µg DNA transfected using lipofectAMINE into 1 X 25cm ² flask (precoated with collagen) of POME cells
	Day 1	Transfected cells plated onto 6 X 10cm diameter petri dishes and 0.8 mg/ml G418 selection applied
	Day 14-17	G418 resistant colonies picked to collagen coated 6-well dishes
	Day 21-25	Samples taken for PCR analysis, clones cryopreserved

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The PCR scheme used to identify POME cells which had undergone a gene targeting event was based on the use of one primer which hybridised to a region within the IRES region of BLAT3 (primer COLTPCR8) and one which hybridised to a region of the BLG promoter not contained within the vector (primer BLAT3-3). The approximate position of these primers is shown in Figure 11 and the sequence of each primer was as below:

BLAT3-3: TAAGAGGCTGACCCCGGAAGTGTT

COLTPCR8: GACCTTGCATTTCCTTTGGCGAGAG

Samples of cells to be screened were lysed in PCR lysis buffer (50mM KCl, 1.5 mM MgCl₂, 10mM Tris pH8.5, 0.5% NP40, 0.5% Tween) plus Proteinase K, and incubated at 65°C for 30min. Proteinase K was inactivated at 95°C for 10 min and polymerase chain reaction carried out using the "Expand long template PCR system" (Boehringer) following the manufacturers recommended conditions. The thermal cycling conditions were as below:

	94°C	2 min
10 cycles of		
	94°C	10 sec
	60°C	30 sec
	68°C	2 min
20 cycles of		
	94°C	10 sec
	60°C	30 sec
	68°C	2 min + 20 sec/cycle
	68°C	5 min

Figure 12 shows an agarose gel electropherogram of PCR products amplified from 16 G418 resistant BLAT-3 transfected POME cell clones. One of these (clone 3) shows the presence of the diagnostic 2.375 kb fragment indicative of integration of the IRES neo gene into the BLG locus by homologous recombination.

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Example 6.

Knockout of the alpha 1,3 galactosyltransferase gene locus in primary porcine fetal fibroblasts by homologous recombination.

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A primary obstacle in xenotransplantation is the occurrence of hyperacute rejection (HAR) which destroys vascular endothelial cells in the donor organ by a complement-dependent mechanism. A carbohydrate antigen, Gal $\alpha 1 \rightarrow 3$ Gal, has been identified as the major antigen responsible for HAR (Sandrin et al., Transplant Rev 8, 134-139, 1994). Although most mammals have the Gal $\alpha 1 \rightarrow 3$ Gal structure, it is lacking in humans, and human sera have potent antibodies against the antigenic epitope (Galili et al., J Exp Med 160, 1519-1531, 1984). The antigenic carbohydrate structure is formed through the action of an enzyme, α 1,3-galactosyltransferase, which transfers galactose from UDP-galactose to *N*-acetyllactosamine (Gal $\beta 1 \rightarrow 4$ G1cNAc), yielding Gal $\alpha 1 \rightarrow 3$ Gal $\beta 1 \rightarrow 4$ G1cNAc. Alpha1,3-galactosyltransferase knockout mice have been generated and cells from these mice are less susceptible to cytotoxic attack by human sera (Tearle et al., Transplantation, 61, 13-19, 1996). These results indicate that removal of α 1,3-galactosyltransferase activity in porcine cells or organs should dramatically reduce HAR when these tissues are used for xenotransplantation. The porcine α 1,3-galactosyltransferase cDNA has been cloned and transfection analysis confirmed that these clones encoded functional α 1,3-galactosyltransferase (Sandrin et al., Xenotransplantation 1, 81-88, 1994). Recently, the porcine α 1,3-galactosyltransferase (GT) full length cDNA (3.2 Kb) has been cloned and its genomic organisation (6 exons encompassing a 24 kb region) has been reported (Katayama, A

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et al, Glycoconjugate J , 15, 583-589, 1998). The goal was to knockout the α 1,3 GT gene in primary porcine cells by homologous recombination, and use the knockout cells as nuclear donors for somatic cell nuclear transfer to produce GT-deficient pigs.

5 Isolation of Primary Porcine PFF4 fetal fibroblasts

A porcine fetus (Large White x Yorkshire cross) at 33 days gestation was prepared for cell isolation by first removing the head and entrails, washing three times with DMEM, and then mincing the remaining fetal tissue into about 20 ml of DMEM with sterile scissors. Finely minced tissue was then transferred to a 50 ml polypropylene centrifuge tube, and spun to remove the DMEM. The tissue was then digested with collagenase (100u/ml in 40 ml), for 1 hr. at 37°C in a shaking water bath. Tissue clumps were broken apart with vigorous pipetting, and the resulting cell suspension was spun to remove the collagenase solution. The digested cell suspension was then plated in three T-75 flasks in DMEM + 10%FBS + non-essential and essential amino acids. Cells were confluent in two days, and were passaged into six T-75 flasks. After two days, the flasks were harvested, and the cells frozen in 100 1 ml cryovials.

Construction of the porcine α -1,3 GT knockout vector (pPL501).

Cells from the primary fetal fibroblast culture, PFF4, were used for genomic DNA isolation. Genomic DNA from PFF4 cells was used to PCR clone isogenic α -1,3 GT DNA sequences for use in construction of a porcine α -1,3 GT knockout vector. The knockout vector was designed as a replacement-type vector, incorporating more than 10 kb of homology, in order to maximise the frequency of recombination. Since the α -1,3 GT gene is expressed in fibroblast cells, a promoter trap strategy was utilised to enrich for homologous recombination events.

The porcine α 1,3 GT promoter-trap knockout vector, pPL501, was constructed from the following three components (figure 13):

- (1) The 5' recombination arm consists of a 9 kb PCR-generated genomic sequence, from the $\alpha 1,3$ GT gene, from porcine primary fetal fibroblasts (PFF4) cells; which consists of 64 base pairs from the 3' end of exon 4, extending from intron 4 to intron 6, and including 81 base pairs from the 5' end of exon 7; The PCR primers used to clone this 9 kb region were as follows:

GAGTGGTTCTGTCAATGCTGCT (5')

GGAAGCTCTCCTCTGTTGTCTT (3')

- (2) A promoter-less selectable neo marker consisting of a 2.057 kb BamHI-XhoI fragment, containing the IVS-IRES-neo-BGHpA expression cassette, (from pIRESneo; Clontech; GenBank Accession #U89673)

- (3) A 3' recombination arm consisting of a 1.8 kb PCR-generated $\alpha 1,3$ GT sequence from exon 9 (starting 84 bp from the 5' end of exon 9, and extending 1844 bp to the 3' end of exon 9), also from PFF4 cells. The PCR primers used to clone this 1.8 kb sequence were as follows:

GGTGGATGATATCTCCAGGATGCCT (5')

GCTGTTTAGTCATGAGGACTGGGT (3')

Random integration of the promoter trap construct does not confer G418 resistance. Homologous recombination results in insertion of the promoterless neo gene, into exon 7, downstream of the endogenous $\alpha 1,3$ GT promoter, allowing transcription of a bicistronic message. Translation of the neo coding region, from the targeted locus, initiates at the internal ribosome entry site. Homologous recombination results, not only in insertion of the IRES-neo cassette into exon 7, but deletion of exon 8, thus interrupting the $\alpha 1,3$ GT coding region, and creating a null allele. During construction of the pPL501 vector, sequencing of the 5' junction of the 9 kb homology region, revealed a sequence polymorphism. It was not known if this was a natural polymorphism between the two PFF4 $\alpha 1,3$ GT alleles, or a PCR error, therefore, a

second knockout vector, pPL502 was made that is identical to pPL501, except using the polymorphic 9 kb 5' recombination arm. Both pPL501 and pPL502 were used, in equimolar amounts, for transfections.

5 Transfection of Primary PFF4 cells with the alpha-1,3 GT targeting vector.

Equimolar amounts of the pPL501/502 knockout vectors were transfected in supercoiled and covalently closed circular form into early passage PFF4 cells and G418 resistant clones were isolated as summarised below:

- | | | |
|----|------------|---|
| 10 | Day 0: | PFF4 cells at passage 3 were seeded in a 75cm ² flask at 40% confluence. |
| 15 | Day 1: | After 24 hours PFF4 cells were at 80% confluence, and transfected with 8µg pPL501/502 DNA using 40 µl GenePORTER reagent following the procedure recommended by the manufacturers (Gene Therapy Systems). |
| 20 | Day 2: | Transfected cells were split into eight 48 well plates and eight 24 well plates in medium containing 350µg/ml G418 |
| 25 | Day 16: | 94 G418 ^R colonies were isolated and re-plated into 12 well dishes. 45 of the best-growing colonies were sampled for PCR analysis. |
| 30 | Day 20-25: | Colonies were expanded into 25cm ² flask. |
| | Day 25-31: | Expanded colonies were cryopreserved. |

Throughout, PFF4 cells were grown in DMEM supplemented with Non-Essential Amino Acids (1X), basic fibroblast growth factor (2ng/ml), 10% fetal calf serum in standard tissue culture flasks and dishes, in a humidified tissue culture chamber using

an atmosphere composed of 5%O₂, 5%CO₂, and 90% N₂. Cells were passaged by standard trypsinisation.

5 PCR analysis was performed to screen potential recombinants, using primers designed to distinguish between random integrants and homologous recombinants. The sequence of these primers is shown below.

Neo442s: CATCGCCTTCTATCGCCTTCTT (5')
Alpha-Gte9a2: AGCCCATCGTGCTGAACATCAAGTC (3')

10

The Neo442s primer was designed to bind with sequences in the 3' end of the neo gene; while the alpha-gte9a2 primer binds to sequences in GT exon 9 outside the region included in the targeting vector. The positions of these primers relative to the predicted structure of the targeted locus is shown in Figure 14.

15

Cells were harvested from 45 G418^R colonies for PCR screening, and were lysed in PCR lysis buffer (40mM Tris-HCl pH8.9, 0.9% Triton X-100, 0.9% Nonidet P40, 400µg/ml proteinase K) at 50°C for 15 minutes. 5 µl of lysed cells (~2-5000 cells) were incubated at 65° C for 15 minutes, followed by Proteinase K inactivation at 95° C for 10 min. PCR amplification was performed using "Expand High Fidelity" Taq polymerase (Roche Molecular Biochemicals) following the manufacturers recommended conditions. The thermal cycling conditions were as below:

20

25

94 °C 2 min

30 cycles of

94 °C 15 sec

64 °C 30 sec

68 °C 4min (with 20sec/cycle increasing time increments
in cycles 10-30)

30

72 °C 7 min

Amplification of a 2.4kb product (the 3' end of which originates in the endogenous gene) indicated that construct integration was due to homologous recombination at the correct site within the α 1,3 GT locus. Fifteen out of 45 G418^R colonies (33%) showed the presence of the 2.4 kb PCR fragment, diagnostic of a targeted recombination event. PCR products from four independent colonies were subcloned into the pCR-XL-TOPO vector and sequenced to verify recombination. Results illustrated in Figure 15 demonstrate that the sequences from the 3' end of each of the PCR products sequenced corresponded to the sequence expected of correct homologous recombination.

These α -1,3 GT knockout cells will now serve as nuclear donors for somatic cell nuclear transfer towards the production of pigs deficient in the α 1,3 galactosyl transferase enzyme.

Example 7

Knockout of bovine β -lactoglobulin (BLG) gene locus in primary bovine fetal fibroblasts (HFF5) by homologous recombination

Bovine β -lactoglobulin (BLG) is one of the major allergens involved in human allergic responses to cow's milk proteins. Knockout of the BLG gene in cow cells, in combination with somatic cell nuclear transfer, to produce a BLG-deficient cow, and subsequently BLG-free milk, presents the opportunity to make a less allergenic and more human-like infant formula.

The bovine BLG genomic DNA and cDNA have been cloned (Hytinen et al, J Biotechnol, 61, 191-198, 1998; Alexander et al, Nucleic Acids Res, 17, 6739, 1989).

Using sequence information from GenBank (GenBank Accession # Z48305), portions of the BLG gene were recloned from primary bovine fetal fibroblast cells, for use in construction of the BLG knockout vector. Since the BLG gene is not expressed in primary fetal fibroblasts, the BLG knockout vector was designed to incorporate a polyA-trap strategy to enrich for homologous recombination events.

Isolation of primary bovine HFF5 fetal fibroblasts

An elite Holstein male fetus at approximately 55 days gestation was collected from a local abattoir and prepared for isolation. The fetus was first removed from the placental membranes and then washed three times with Dulbecco's modified Eagles medium (DMEM) at room temperature. In a fresh 20ml aliquot of DMEM, the surface skin and subdermal tissue was stripped from the skeletal structure using small scissors and then diced as finely as possible. Minced tissue was then spun down and the DMEM was replaced with 50 ml of collagenase at 100units per ml of DMEM. Tissue was digested for 1 hr in a 37°C water bath. Minced tissue was then broken apart with repeated pipetting and the resulting cell suspension was spun to remove the collagenase solution. The cell pellet was then resuspended in complete DMEM plus 10% fetal bovine serum, non essential amino acids (1X) and basic fibroblast growth factor (2ng/ml) plus gentamycin. Cells were seeded into 4 T-75 flasks. Resulting cells were confluent and frozen three days post isolation.

Poly A-trap Knockout Vector Construction

The bovine BLG polyA-trap knockout vector pPL522 was constructed from the following three components (see figure 16):

(1) The 5' recombination arm consists of a 10 kb PCR-generated genomic sequence comprising the BLG promoter region through to 89bp downstream from the first ATG in exon 1, derived from DNA isolated from primary Holstein fetal fibroblasts (HFF5). The primers used to generate the PCR fragment were:

BoBLGpro: 5' CCA GTG CTG ATT TGA TTT CCT ACT CAC GCC 3'

BoBLGpro7: 5' ACC TTC TGG ATA TCC AGG CCC TTC ATG GTC 3'

(2) A poly A-less selectable marker comprising a 1415bp Xho I – Sma I fragment containing the mouse phosphoglycerate kinase (PGK) promoter, and a neo gene cassette without a poly' A signal, from pPL442 which was derived from pKOTKneoV904 (Lexicon Genetics Inc., Woodlands, Texas);

(3) The 3' recombination arm is a PCR-generated 1935 bp Nco I-BamH I fragment of BLG genomic sequence (GenBank Accession # Z48305) from HFF5 cells. This 3' arm contains BLG sequences comprising 114bp from the 3' end of exon 2, intron 2, exon 3 and 885bp from the 5' end of intron 3.

Transfection of Primary HFF5 cells with the BLG knockout vector

HFF5 cells were maintained at 37°C, with 5% CO₂, in DMEM medium supplemented with 10% Fetal calf serum, Non-Essential Amino Acids (1X), and basic fibroblast growth factor (2ng/ml). The selection medium contained 350µg/ml (active concentration, Gibco-BRL) of G418.

BLG knockout vector pPL522 DNA was transfected without linearisation by restriction digestion (supercoiled and closed circular form) into HFF5 cells by lipofection, using GenePORTER (Gene Therapy Systems), and the G418 resistant colonies were selected as follows:

Day 0: HFF5 cells at passage 1 (1 million cells per vial) were thawed from liquid nitrogen and seeded into a 25cm² flask

Day 1: Cells at approximately 60% confluence were transfected with 2 ml of transfection media containing 1 µg of undigested pPL522 DNA (>70% supercoiled) and 20 µl of GenePORTER reagent. Cells were incubated in 5% CO₂ at 37° C. After 4 hours, 2ml of growth medium (DMEM + 20% FCS) was added.

Day 2-12: Transfected cells were trypsinised at 24 hrs post transfection and seeded into 24 well plates at a density of 2500 to 5000 cells per well in selection medium with 350 µg/ml of G418. Cells were incubated in 5% CO₂ at 37° C. Medium was changed every 3 days during selection.

5

Day 13-15: Eighty-five colonies were passed from 24 well plates to 12 well plates. Wells which contained more than one distinguishable colony were harvested as pools (8 to 12 colonies per pool). A total of 21 pools were submitted for PCR analysis.

10 Day 15-17: Fifty-two well-isolated, single colonies from 12 well plates, upon reaching confluence, were passed to 60mm dishes. An aliquot of each colony was submitted for PCR analysis.

15 Day 17-22: The remaining cells from each of the 52 single colonies were frozen (2 vials for each colony), and stored at -70° C.

PCR screening of G418 resistant colonies

G418 resistant colonies and pools were screened by PCR analysis, using primers designed to distinguish between random integration and homologous recombination events (Figure 17). The 5' primer (Neo442s) binds to the 3' end of the neo gene within the knockout vector. The 3' primer (BLG3'1) binds to a region of bovine BLG exon 4 which is outside of sequences present in the knockout vector (approximately 260 bp 3' of the 3' end of the BLG 3' homologous arm in the vector. The primer sequences are shown below:

25

Neo442s: 5' CAT CGC CTT CTA TCG CCT TCT T 3'

BLG3'1: 5' CCA GCA CAA GGA CTT TGT TCT C 3'

30 Cells were lysed in PCR lysis buffer (40mM Tris-HCl pH8.9, 0.9% Triton X-100, 0.9% Nonidet P40, 400µg/ml proteinase K) at 50° C for 15 minutes. Five µl of lysed

cells (5000-10000 cells) were incubated at 65°C for 15 minutes, followed by proteinase K inactivation at 95°C for 10 minutes. PCR amplification was performed using Expand High Fidelity Taq (Roche Molecular Biochemicals) and the manufacturer's protocol with the following thermal cycling program:

- 5 94°C 1 minute
- 60°C 1 minute
- 72°C 2 minutes
- 35 cycles

10 Amplification of a 2.3kb product (the 3' end of which originates in the endogenous gene, not the construct) indicates that construct integration was due to homologous recombination within the BLG locus.

Subcloning and sequencing of PCR products

15 Out of 52 single colonies and 21 pools (each pool comprising 8 to 12 colonies), 5 single colonies (9.6%) and 17 pools (81%) showed positive PCR products. PCR products from 3 single colonies were subcloned into the pCR-XL-TOPO vector (Invitrogen), and two subclones from each of the 3 single colonies (6 clones total) were sequenced, generating more than 400bp of sequence from both ends. Sequencing results showed that all subclones matched the sequence expected after correct

20 homologous recombination (Figure 18).

25 Having described the preferred embodiments of the present invention, it will be clear to those ordinarily skilled in the art that various modifications may be made to the disclosed details and embodiments and that such modifications are covered by the scope of the present invention.